



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165011

TO: Joseph Weitach
Location: REM/2d51/2c18
Art Unit: 1632

Sept 12, 2005

Case Serial Number: 09/655109

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 07:52:31 ; Search time 3609.35 seconds
(without alignments)
9987.065 Million cell updates/sec

Title: US-09-655-109A-4
Perfect score: 947
Sequence: 1 accanaccacaaagaga.....tggtctcgagatctatga 947

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_hcc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854.8	90.3	895	7 CK230944	ILLUMIGEN
2	783.8	82.8	932	1 AJ816315	AJ816315
3	730	77.1	1436	3 AK033024	Mus muscu
C 4	724.8	76.5	799	7 CK774847	CK774847 963641 MA
C 5	711.8	75.2	736	5 BM985193	BM985193 UI-CF-EC1
6	673	71.1	707	5 BX924636	BX924636 BX924636
C 7	656	69.3	726	7 CK777039	CK777039 964031 MA
C 8	648.4	68.5	662	5 BQ015219	BQ015219 UI-H-ED1-
C 9	637.2	67.3	664	7 CK299391	UI-E-EU1-
C 10	631.2	66.7	650	5 BQ189224	BQ189224 UI-E-EU1-
C 11	617.6	65.2	642	2 BF116048	BF116048 7n76g08.x
C 12	613.2	64.8	621	1 A1627241	ty72a11.x
13	607.2	64.1	792	7 CN533672	UI-M-HO0-
14	604.8	63.9	784	7 CK635466	UI-M-HN0-
15	593	62.6	654	9 AY400131	Homo sapi
16	589.6	62.3	769	6 CK324092	UI-M-FY0-
17	585.2	61.8	751	6 CK324087	UI-M-FY0-
18	580.2	61.3	639	6 CB444569	695860 MA
19	580.2	61.2	745	6 CD355761	UI-M-FY0-
C 20	575.2	60.7	618	4 BM312863	ig80c01.x
C 21	574.4	60.7	723	7 CN457401	UI-M-HN0-
C 22	570.6	60.3	573	1 A1693196	wd68f05.x
C 23	568.6	60.0	610	6 CB287220	CMD55_C02

C 25	552	58.3	618	6	CB461283	CB461283 721237 MA
C 26	551	58.2	573	1	AI912660	AI912660 wsl2c06.x
C 27	549.2	58.0	589	6	CB287224	CMD55_C09
C 28	546.6	57.7	548	2	AW193683	xm29d02.x
C 29	546.6	57.7	564	6	CB854840	UI-CF-EC1
C 30	546	57.7	576	1	AI693651	wd79f12.x
31	543	57.3	703	7	CK639892	UI-M-HN0-
32	543	57.3	703	7	CN526226	UI-M-HN0-
33	542.8	57.3	798	5	BU704183	UI-M-FOO-
34	541	57.1	700	7	CK640200	UI-M-HN0-
35	540.2	57.0	814	9	CG498682	OST40156
C 36	539.2	56.9	547	1	AA725613	ai19d09.s
37	538.4	56.9	506	4	BI553612	603190533
38	537	56.7	695	5	BQ444213	UI-M-EX0-
39	536.2	56.6	770	9	CG499356	OST41345
C 40	535.4	56.5	539	2	BE464892	hv95d04.x
41	534.6	56.5	699	7	CO045489	UI-M-HO0-
42	534.6	56.5	839	6	CB989163	AGENCOURT
43	533.4	56.3	1940	3	CR603956	full-leng
44	533	56.3	778	3	CR626146	full-leng
45	531.2	56.1	604	6	CA751459	UI-M-FOO-

ALIGNMENTS

RESULT 1
CK230944
LOCUS
DEFINITION ILLUMIGEN MCQ 1331 Katze_MMP12 Macaca mulatta cDNA 5' similar to human RYBP (Hs_7910), mRNA sequence.
895 bp mRNA linear EST 09-DEC-2003
ACCESSION CK230944
VERSION CK230944.1 GI:39637302
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 895)
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.10.17. 765 Q20 bases. Assemblies in contig w/ 1 member(s). Contig contains 1 (0%) lib members.
PCR Primers
FORWARD: CCCTCACTAAGGGACAAA
BACKWARD: CACTATAGGCGAATTGGTA
Insert Length: 895 Std Error: 0.00
Plate: CL000013 row: C column: 06
Seq primer: CCCTCACTAAGGGACAAA
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1. .895
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/sex="male"
/dev_stage="newborn infant"
/lab_host="E. coli SOLR"
/clone_lib="Katze MMP12"
/notes="Organ: placenta; Vector: Uni-ZAP XR; Site 1: EcoR I; Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis kit (catalog #20400) and ZAP-cDNA Gigapack III Gold Cloning Kit (Catalog #200450)"

ORIGIN

```
Query Match      90.3%; Score 854.8; DB 7; Length 895;
Best Local Similarity 98.8%; Pred. No. 4.2e-217;
Matches 859; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 52 CCGAAACAGTGTGAGACCTTTAAATCAGCATCTCGATGTGAGGAAAGCCACTCCAC 111
    |||||
DB 9 CAGNAACAGTGTGAGACCTTTAAATCAGCATCTCGATGTGAGGAAAGCCACTCCAC 68

QY 112 CAGAAACCTCGGATCAATTTCTCAGCTGGTGGNCACAAAGATGGCACAA CAGTATGGCAC 171
    |||||
DB 69 CAGAAACCTCGGATCAATTTCTCAGCTGGTGGCACAAAGTGGCAC CAGCATGTGGCAC 128

QY 172 CCACACACCCCTTAAAGAGAGAGAGAGAGAGTGAAGAGCAGACAGAGAGAAC 231
    |||||
DB 129 CCCACACCCCTTAAAGAGAGAGAGAGAGTGAAGAGCAGACAGAGAGAAC 188

QY 232 TGAGAAAGACAGGAAATTTAGTCTCTAGTGTATCCAGAAATAATACCAAGAGAAACCAA 291
    |||||
DB 189 TGAGAAAGACAGGAAATTTAGTCTCTAGTGTATCCAGAAATAATACCAAGAGAAACCAA 248

QY 292 ACCAAAGTGTGACATTTCTGAAAGATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAA 351
    |||||
DB 249 ACCAAAGTGTGACATTTCTGAAAGATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAA 308

QY 352 TGCTACAAACAGACGAGCGAACAATTCACCTCAAGGCCCGCGTGAAGAAACGTGGA 411
    |||||
DB 309 TGCTACAAACAGACGAGCGAACAATTCACCTCAAGGCCCGCGTGAAGAAACGTGGA 368

QY 412 CAGGAGCACTGCACAGCAGTTGGCAGTAATCTGTGGGCAACGTCAACCGTCATTTATCACAGA 471
    |||||
DB 369 CAGGAGCACTGCACAGCAGTTGGCAGTAATCTGTGGGCAACGTCAACCGTCATTTATCACAGA 428

QY 472 CTTTAAAGAAAGACTCGCTCTCATCGACATCTCTCATCACAGTGCACCTCCAGTGCAGG 531
    |||||
DB 429 CTTTAAAGAAAGACTCGCTCTCATCGACATCTCTCATCACAGTGCACCTCCAGTGCAGG 488

QY 532 GTGAGACAGCAGACAGACAGTCTGGGTGAGAGAGCAGACAGAGGGCTCCTCCCG 591
    |||||
DB 489 GTGAGACAGCAGACAGACAGTCTGGGTGAGAGAGCAGACAGAGGGCTCCTCCCG 548

QY 592 TTCTCTCCAGCCAAAGGGCGACATGTGACGAGTCAATGATGAATCTTTCTGAAATGTCAC 651
    |||||
DB 549 TTCTCTCCAGCCAAAGGGCGACATGTGACGAGTCAATGATGAATCTTTCTGAAATGTCAC 608

QY 652 ATGGAATTTGAAACCTATGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCT 711
    |||||
DB 609 ATGGAATTTGAAACCTATGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCT 668

QY 712 GCTTGCATCCCTGGAGATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAA 771
    |||||
DB 669 GCTTGCATCCCTGGAGATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAA 728

QY 772 TTTCTGTCTGGCATGGGCATCTGGCCACCAAGGAATTTGCAACCTCGACGATTAATCTTG 831
    |||||
DB 729 TTTCTGTCTGGCATGGGCATCTGGCCACCAAGGAATTTGCAACCTCGACGATTAATCTTG 788

QY 832 ACACCTTTTATGATTTCCATGTTTTTATATGATTTTCTTAACAATCATTTATTAATGGATG 891
    |||||
DB 789 ACACCTTTTATGATTTCTGTTTTTATATGATTTTCTTAACAATCATTTATTAATGGATG 848

QY 892 TGCTCCTGAAATCTACTTTTATAAAAAA 920
    |||||
DB 849 TGCTCCTGAAATCTACTTTTATAAAAAA 877

RESULT 2
AJ816315
LOCUS
DEFINITION AJ816315 KN206 Bos sp. cDNA clone C0005210i11, mRNA sequence.
ACCESSION AJ816315
VERSION AJ816315.1 GI:51883791
KEYWORDS EST.
```

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SOURCE Bos sp.
ORGANISM Bos sp.
          Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovinae; Bos.
REFERENCE 1 (bases 1 to 932)
AUTHORS McGuire,K. and Glass,E.J.
TITLE Unpublished ESTs, McGuire and Glass
JOURNAL Unpublished (2004)
COMMENT Contact: McGuire K
          Genomics and Genetics
          Roslin Institute
          Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source            1..932
                        /organism="Bos sp."
                        /mol_type="mRNA"
                        /db_xref="taxon:29061"
                        /clone="C0005210i11"
                        /tissue_type="blood"
                        /cell_type="bovine monocyte"
                        /clone_lib="KN206"
     note="Vector: pBluescriptII (SK+); Site 1: EcoRV (lost);
          Site 2: NotI; Normalised library constructed from pooled
          monocytes from Bos taurus (Holstein) and Bos indicus
          (Sahiwal) cattle subjected to various stimuli, including
          infection with the protozoan parasite Theileria annulata"
```

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ORIGIN
Query Match      82.8%; Score 783.8; DB 1; Length 932;
Best Local Similarity 92.1%; Pred. No. 4e-198;
Matches 846; Conservative 1; Mismatches 70; Indels 2; Gaps 2;

QY 3 CANACCCAAAAAAGAGATCTGGAATTCGATCTCTGAGGCCACGAAGCCGAAACAGTG 62
    |||||
DB 2 CAAAACCTGCGCAGACGAAGGCTTTTGGGATTTGTAGCGTCTGCACCTTCAGAAACAGCG 61

QY 63 CTGAAGCCTTTAATTCAGCATCTCGATCTGAGGAAAGCAGCCTCCACAGAAACCTC 122
    |||||
DB 62 CCGAAGCCTTTAATTCAGTATCTGCGATGTGAGAAAGGGCAGCTCCACAGAAACCTC 121

QY 123 GGATCAATTTCTCAGCTGGTGGCNCAACAAGTGGCACACAGATATGCCACCCACCC 182
    |||||
DB 122 GGATCAATTTCCAGCTGGTGGCACAGCAGTGGCCAGCAGTATGCCACTCCACCC 181

QY 183 CTAAAAAGGAGAAAGAGAAAGTTGAAAAAGCAGGACAAAGAGAAACCTTGAGAAAGACA 242
    |||||
DB 182 CTAAAAAGGAGAAAGAGAAAGTTGAAAAACAAAGACAAAGAGAAACCTTGAGAAAGATA 241

QY 243 AGGAATTTAGTCTAGTGTGTACCAAGAAATACCAAGAAACCAACCAACCAAGTCTG 302
    |||||
DB 242 AAGAAATTTAGTCTAGTGTGTACCAAGAAATACCAAGAAACCAACCAACCAAGTCTG 301

QY 303 ACATTTCTGAAAGATCTCTCTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACACAA 362
    |||||
DB 302 ATATTTCTGAAAGATCTCTCTAGCGAAGTGNACAGTATACAGTCTGCAAAATGCTACACAA 361

QY 363 AGACGAGCGAAACAAATTCACCTCAAGGCCCGCGTGAAGAAACGTTGAGACAGACGCTG 422
    |||||
DB 362 AGACGAGTGAACGAATTCACCTCAAGGCCCGCGTGAAGAAACGTTGAGACAGACCG 421

QY 423 CACAGCAGTTGGCAGTAACCTGTGGGCAACGTCAACCGTCAATTATCACAGACTTTTAAGGAA 482
    |||||
DB 422 CACAGCAGTTGGCAGTACTGTGGGCAACGTCAACCGTCAATTATCACAGACTTTTAAGGAA 481

QY 483 AGACTCGCTCCTCATCGACATCTCTATCCACAGTGCAGTGCAGGGTCAAGACAGC 542
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Qy 28 TTGGATCTCTCGAGGCCACGAGCGGAAACAGTGTGTAAGCCTTTAAATGCAGCATCTG 87
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Qy 192 TTGGATTTGAGCTCTGACCTTTTAGAAACAGCGCGAAGCCTTTAAATGCGACATCTG 251
Db |||||
Qy 88 CGATGTGAGGAAGGCACTCCACCCAGAAAAACCTCGGATCAATTTCTCAGCTGGTGGCNCA 147
Db |||||
Qy 252 CGATGTGCGGAAGGCACTCCACCCAGAAAAACCTCGCATCAATTTCTCAGCTGGTGGACA 311
Db |||||
Qy 148 ACAAGTGGCAACAAGTATGCGACCCCAACACCCCTTAAAGAGGAGAAAGAGAAAGT 207
Db |||||
Qy 312 GCAGGTGGCAACAGCAGTACGCCACTCCACCTCCCTTAAAGAGGAGAAAGAGAGGT 371
Db |||||
Qy 208 TGAAGACGACGACAAAGAGAAACCTGAGAAGACAGGAAATTAGTCTAGTGTACCAA 267
Db |||||
Qy 372 CGAAAGCCTTGACAAAGAAAGCCAGAGAAAGACAGGACATTAGCCCCAGTGTACCAA 431
Db |||||
Qy 268 GAAAAATACCAACAAAGAAAAACCAACCAAAAGTGTGACATTTCTGAAAGATCCTCTAGTGA 327
Db |||||
Qy 432 GAAAAACACCAACAAGAAACAAACCAAAAGTCTGATATTTCTGAAAGATCCTCTAGTGA 491
Db |||||
Qy 328 AGCAACAGCATACAGTCTGCAATGTCTACAACAAGACAGGCAAAACAAATCACACCTC 387
Db |||||
Qy 492 AGCTAACAGCATACAGTCTGTAACGCTACAACAAGACAGGCAAAACCAACACACCTC 551
Db |||||
Qy 388 AAGCCCCGGCTGAAAAACCTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACTGTGG 447
Db |||||
Qy 552 AAGCCCCGGCTGAAGAAATGTGACAGAGGACCGCACAGATGTGGCAGTAACTGTGG 611
Db |||||
Qy 448 CAACGTCACCGCTCATTTATCACAGACTTTAAGGAAAAAGACTCGCTCTCATCGACATCCTC 507
Db |||||
Qy 612 CNAAGTCACCGCTCATTTATCACAGACTTTAAGGAAAAAGACTCGCTCTCTCCACATCCTC 671
Db |||||
Qy 508 ATCCACAGTCACTCCAGTGCAGGCTGAGAACAGAGCAACAGACGACGCTCGGGGTGAGA 567
Db |||||
Qy 672 TTCCACAGTCACTCCAGTGCAGGCTGAGAACAGAGCAACAGACGACGCTCGGGCTCAGA 731
Db |||||
Qy 568 GAGCACAGACAGGCTCTCCGCTTCTCCAGCCAAAGGGCGACATGTCAGCAGTCAA 627
Db |||||
Qy 732 GAGCACAGACAGGCTCTCCGCTTCTCCAGCCAAAGGGCGACATGTCAGCAGTCAA 791
Db |||||
Qy 628 TGATGAATCTTTCTGAAATTTGCATGGAATTTGTGAAATCTATGAATCAGGGTATGAAAT 687
Db |||||
Qy 792 TGAATGAATCTTTCTGAGATTTGCATGGAATTTGTG-AAACTGAATCAGGGTATGAGAT 850
Db |||||
Qy 688 TCAAAACCTCCACTCGCCATGCTGCTTGTGATCTCCGGAATCTTCTGTGGACATCGAC 747
Db |||||
Qy 851 TCAAAACCTCCACTCGCCATGCTGCTTGTGA-CCCTGGAGAGTCTTCTGTGGA---CGAC 906
Db |||||
Qy 748 CTCTTAGTATGCTGCCAGGATATTTCTGCTTGGCATGGGCATCTGGCCACCAAGGAAT 807
Db |||||
Qy 907 CTTGTAGTGACGCTTACCAGAGAGGTTCCGCTTGGCGTGGGCATCTGGCTTACCAGGAAT 966
Db |||||
Qy 808 TTGCGACCTCGACGATTTACTCTTGACACTTTTATGATTTTCCATTTGTTTATATGATTTTC 867
Db |||||
Qy 967 TTGCTACCTCGACGATTTACTCTTGACACTTTTATGATTTTCCATTTGTTTATATGATTTTC 1026
Db |||||
Qy 868 CTAACAATCATTTTATATATGATGCTCTCGAATCTACTTTTATATATATATATATATATA 920
Db |||||
Qy 1027 CTAACAATCATTTTATATATGATGCTCTCGAATCTACTTTTATATATATATATATA 1079
Db |||||
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RESULT 4
CK774847/c
LOCUS 799 bp mRNA linear EST 20-FEB-2004
DEFINITION 963641 MARC 2Bov Bos taurus cDNA 3', mRNA sequence.
ACCESSION CK774847
VERSION CK774847.1 GI:42728990
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
```

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REFERENCE
AUTHORS
Smith, P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casae, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chicko-Mckown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
TITLE
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 105 row: P column: 12
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers
1..799
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2Bov"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
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Query Match 76.5%; Score 724.8; DB 7; Length 799;
Best Local Similarity 94.9%; Pred. No. 2.3e-182;
Matches 758; Conservative 1; Mismatches 39; Indels 1; Gaps 1;
Qy 116 AAACCTCGGATCAATTTCTCAGCTGGTGGCNCAACAGTGGCAACAAGTATGCCACCCA 175
Db |||||
Qy 799 AAACCTCGGATCAATTTCCAGCTGGTGGCAACAGTGGCCCGCAGCAGTATGCCACTCCA 740
Db |||||
Qy 176 CCACCCCTTAAAGAGAGAGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 235
Db |||||
Qy 739 CCACCCCTTAAAGAGAGAGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 680
Db |||||
Qy 236 AAAGCAAGGAAATTAAGTCTCTAGTGTTCACAGAAAAATACCAACAGAAAAACCAACCA 295
Db |||||
Qy 679 AAGATTAAGAAATTAAGTCTCTAGTGTTCACAGAAAAATACCAACAGAAAAACCAACCA 620
Db |||||
Qy 296 AAGTCTGACATTTCTGAAAGATCCTCTAGTGAAGCAACAGCATACAGTCTGCAATGCT 355
Db |||||
Qy 619 AAGTCTGATATTCTGAAAGATCCTCTAGCAGATGCAACAGTATACAGTCTGCAATGCT 560
Db |||||
Qy 356 ACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 415
Db |||||
Qy 559 ACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
Db |||||
Qy 416 AGCAGTGCACAGCAGTGGCAGTAACTGTGGGCAACGTCACCGCTATTATACAGAGACTTT 475
Db |||||
Qy 499 AGCAGCGCACAGCAGTGGCAGTGAATGTGGGCAACGTCACCGCTATTATACAGAGACTTT 440
Db |||||
Qy 476 AAGGAAAAAGATCGCTCTCTCATGCAATCTCTCATTCACAGTGAACCTCCAGTGCAGGTC 535
Db |||||
Qy 439 AAGGAAAAAGATCGCTCTCTCATGCAATCTCTCATTCACAGTGAACCTCCAGTGCAGGTC 380
Db |||||
Qy 536 GAACAGCAAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
Db |||||
Qy 379 GAACAGCAAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 320
Db |||||
Qy 596 TCACAGCCAAAGGGCGACATGTGACAGTCAATGATGAATCTTTCTGAAATTCACATGG 655
Db |||||
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319 TCCAGGCAAAAGGCGAGCATGTGACGAGTAATGATGAGTCTTTTGAAGTGCACATGG 260
QY AATTGCAAAACTATGATCAGGATGAATTCAAACCTCCACCTGCCATGCTGCTT 715
Db AATTGCAAAACTATGATCAGGATGAATTCAAACCTCCACCTGCCATGCTGCTT 200
QY GCA-TCCTCGGAGATCTTCTGTGGACATCGACTCTTACTGATGCTGCCAGGATAATTT 774
Db GCACCCCTGGGAAATTTCTGTGGACATGACCTTTTGTGATGCTGCCAGGATAATTT 140
QY CTGCTTCCATGGGCACTCTGTGGACATCGACTCTTACTGATGCTGCCAGGATAATTT 834
Db TTGCTTCCATGGGCACTCTGTGGACATCGACTCTTACTGATGCTGCCAGGATAATTT 80
QY CTTTATGATTCATGTTTATATGATTTTCTTAACTATTTATATGATGCTGCCAGGATAATTT 894
Db CTTTATGATTCATGTTTATATGATTTTCTTAACTATTTATATGATGCTGCCAGGATAATTT 894
QY TCCTGAATCTACTTTTAT 913
Db TCCTGAATCTACTTTTAT 1
QY TCCTGAATCTACTTTTAT 1
Db TCCTGAATCTACTTTTAT 1

RESULT 5
BM985193/c
LOCUS BM985193
DEFINITION UI-CF-EC1-acc-m-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-acc-m-16-0-UI 3', mRNA sequence.
ACCESSION BM985193
VERSION BM985193.1 GI:19611497
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-23, >AT rich/Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-acc-m-16-0-UI"
/tissue_type="Lung"
/dev_stages="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
```

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UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(ori)18 tail. The sequence tag for this library is
AAGTGCTTAC.
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 75.2%; Score 711.8; DB 5; Length 736;
Best Local Similarity 99.4%; Pred.No. 6.7e-179;
Matches 713; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 204 AAGTTGAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAATAGTCTAGTGTTA 263
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
726 AAGTGTAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAATAGTCTAGTGTTA 667
QY 264 CCAAGAAAAATACCAACAAAGAAACCAACCAAGTCTGACATCTCTGAAAGATCTCTCTA 323
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
666 CCAAGAAAAATACCAACAAAGAAACCAACCAAGTCTGACATCTCTGAAAGATCTCTCTA 607
QY 324 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGCAAAACAAATCA 383
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
606 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGCAAAACAAATCA 547
QY 384 CTTCAAGGCCCGGCTGAAAGAGTGGACAGGAGCATGCGACAGCAGTGGCAGTAACGTG 443
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
546 CTTCAAGGCCCGGCTGAAAGAGTGGACAGGAGCATGCGACAGCAGTGGCAGTAACGTG 487
QY 444 TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGAGCTCGCTCTCATCGACAT 503
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
486 TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGAGCTCGCTCTCATCGACAT 427
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QY 564 CAGAGAGCAGACAAAGGGCTCTCCGCTTCCTCCAGGCCCAAGGGGGGACATGTCAGCAG 623
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 624 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGTAAGAACTATGAATCAGGGTATG 683
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306 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGTAAGAACTATGAATCAGGGTATG 247
QY 684 AAATTCAAAACCTCCACCTGCCCATGCTGCTGCATCCCTCGGAGAAATCTTCTGTGGACAT 743
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
246 AAATTCAAAACCTCCACCTGCCCATGCTGCTGCATCCCTCGGAGAAATCTTCTGTGGACAT 187
QY 744 CGACCTCTTAGTGAATGCTGCCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAAG 803
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 804 GAATTTGGCACCTGACGATTACTCTTGACACTTTTATGATGATTCATTGTTTATATGAT 863
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66 TTTCTTAAACAATCATTTATTAATTTGGATGCTCTCTGAATCTACTTTTTTATAAAAAA 10

RESULT 6
```

UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (ori)18 tail. The sequence tag for this library is AAGTGCTTAC.

TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 75.2%; Score 711.8; DB 5; Length 736; Best Local Similarity 99.4%; Pred.No. 6.7e-179; Matches 713; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 204 AAGTTGAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAATAGTCTAGTGTTA 263
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
726 AAGTGTAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAATAGTCTAGTGTTA 667
QY 264 CCAAGAAAAATACCAACAAAGAAACCAACCAAGTCTGACATCTCTGAAAGATCTCTCTA 323
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
666 CCAAGAAAAATACCAACAAAGAAACCAACCAAGTCTGACATCTCTGAAAGATCTCTCTA 607
QY 324 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGCAAAACAAATCA 383
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
606 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGCAAAACAAATCA 547
QY 384 CTTCAAGGCCCGGCTGAAAGAGTGGACAGGAGCATGCGACAGCAGTGGCAGTAACGTG 443
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
546 CTTCAAGGCCCGGCTGAAAGAGTGGACAGGAGCATGCGACAGCAGTGGCAGTAACGTG 487
QY 444 TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGAGCTCGCTCTCATCGACAT 503
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
486 TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGAGCTCGCTCTCATCGACAT 427
QY 504 CTTCAATCCACAGTGACCTCCAGTGCAGGGTTCAGAACAGCAGACAGCAGCTCGGGGT 563
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
426 CTTCAATCCACAGTGACCTCCAGTGCAGGGTTCAGAACAGCAGACAGCAGCTCGGGGT 367
QY 564 CAGAGAGCAGACAAAGGGCTCTCCGCTTCCTCCAGGCCCAAGGGGGGACATGTCAGCAG 623
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
366 CAGAGAGCAGACAAAGGGCTCTCCGCTTCCTCCAGGCCCAAGGGGGGACATGTCAGCAG 307
QY 624 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGTAAGAACTATGAATCAGGGTATG 683
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
306 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGTAAGAACTATGAATCAGGGTATG 247
QY 684 AAATTCAAAACCTCCACCTGCCCATGCTGCTGCATCCCTCGGAGAAATCTTCTGTGGACAT 743
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
246 AAATTCAAAACCTCCACCTGCCCATGCTGCTGCATCCCTCGGAGAAATCTTCTGTGGACAT 187
QY 744 CGACCTCTTAGTGAATGCTGCCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAAG 803
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
186 CGACCTCTTAGTGAATGCTGCCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAAG 127
QY 804 GAATTTGGCACCTGACGATTACTCTTGACACTTTTATGATGATTCATTGTTTATATGAT 863
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
126 GAATTTGGCACCTGACGATTACTCTTGACACTTTTATGATGATTCATTGTTTATATGAT 67
QY 864 TTTCTTAAACAATCATTTATTAATTTGGATGCTCTCTGAATCTACTTTTTTATAAAAAA 920
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
66 TTTCTTAAACAATCATTTATTAATTTGGATGCTCTCTGAATCTACTTTTTTATAAAAAA 10

RESULT 6

```

BX924636
LOCUS BX924636 707 bp mRNA linear EST 07-MAY-2004
DEFINITION BX924636 Sus Scrofa library (scan) Sus scrofa cDNA clone
ACCESSION scan0017d.d.20 Sprim, mRNA sequence.
VERSION BX924636
KEYWORDS BX924636.1 GI:41141484
SOURCE EST.
ORGANISM Sus scrofa (pig)

REFERENCE
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,P., Cabau,C., Villegier,S.,
Soares,M., Bonaldo,F. and Hacey,F.
TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosse@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0017 row: d column: 20.

FEATURES
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/clone lib="Sus Scrofa library (scan)"
/notes="tissues: adipose tissue, brain, kidney, liver,
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skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

ORIGIN
Query Match 71.1%; Score 673; DB 5; Length 707;
Best Local Similarity 96.9%; Pred. No. 1.6e-168;
Matches 685; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

Qy 206 GTTGAAGCAGGCAAGAGAAACCTGAGAAAGACAAGGAATTAGTCTTAGTGTACC 265
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Qy 266 AAGAAATATACCAACAGAAACCAACCAAGCTGCACATCTCTGAAGATCTCTTAGT 325
Db 61 AAGAAATATACCAACAGAAACCAACCAAGCTGCATATCTGAAGATCTCACCTAGT 120

Qy 326 GAAGCAACAGCATACAGTCTGCAATGCTACAAAGAACCCAGCAGCAACAAATCACACC 385
Db 121 GAAGCAACAGTATACAGTTCAGCAATGCTCACAACCAAGACCAAGTGAACGAATCACACT 180

Qy 386 TCAAGGCCCGCGTGAAGAAACGTGGACAGAGCACTGCACAGCGATGGGAGTAACCTGTG 445
Db 181 TCAAGGCCCGCGTGAAGAAACGTGGACAGAGCACTGCACAGCAAGTTGGCAGTAACCTGTG 240

Qy 446 GGCACCTGCACCGTCATTATACAGACTTTTAAGGAAAGACTCGCTCTCATGCACATCC 505
Db 241 GGCACCTGCACCGTCATTATACAGACTTTTAAGGAAAGACTCGCTCTCATGCACATCC 300

Qy 506 TCATCCACAGTGACCTCCAGTGCAGGGTTCAGAAACAGCAGAACCCAGACAGCTCGGGGTCA 565
Db 301 TCATCCACAGTGACCTCCAGTGCAGGGTTCAGAAACAGCAGAACCCAGACAGCTCGGGGTG 360

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Qy 566 GAGAGCAGACAGCAGGGCTCTCCGTTCTCCAGCCAAAGGGCCACATGTTCAGCAGTC 625
Db 361 GAGAGCAGACAGCAGGGCTCTCCGTTCTCCAGCCAAAGGGCCACATGTTCAGCAGTA 420

Qy 626 AATGATGAATCTTTCTGAAATTCACATGGAATTTGAAAACTATGAATCAGGGTATGAA 685
Db 421 AATGATGAATCTTTCTGAAATTCACATGGAATTTGAAAACTATGAATCAGGGTATGAA 480

Qy 686 ATTCAAAACCTCCACCTGCCCATGCTGCTTGCAATCCCTGGAGAATCTTCTGTGGACATCG 745
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Qy 746 ACCTCTTAGTATGCTGCCAGGATATTTCTGCTTGGCATGGCATCTGGCCACCAAGGA 805
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Qy 806 ATTTCCGACCCCTGACGATTACTCTTGACACTTTTATGTATTCATTGTTTATATGATTT 865
Db 601 ATTTCCGACCCCTGACGATTACTCTTGACACTTTTATGTATTCATTGTTTATATGATTT 660

Qy 866 TCCTAAACATCATTTATTAATTTGATGATGCTCTCGAATCTACTTTTAA 912
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RESULT 7
CK777039/c
LOCUS CK777039 726 bp mRNA linear EST 20-FEB-2004
DEFINITION 964031 MARC 2BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CK777039
VERSION CK777039.1 GI:42729352
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
AUTHORS Casas,E., Wray,J.B., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 120 row: A column: 12
Seq primer: GTAATACGACTCACTATAGGG.
FEATURES
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/clone lib="MARC 2BOV"
/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semiteendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

ORIGIN

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Tumor Gene Index		Unpublished (1997)		Contact: Robert Strausberg, Ph.D.		Email: cgapbs-remail.nih.gov		Tissue Procurement: Dr. Jose Mercuende		CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa		CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		The following repetitive elements were found in this CDNA sequence: 1-23, >AT rich#Low_complexity		Seq primer: M13 FORWARD		POLYA=Yes.		Location/Qualifiers		1..662		/organism="Homo sapiens"		/mol_type="mRNA"		/db_xref="taxon:9606"		/clone="IMAGE:5834508"		/tissue_type="Chondrosarcoma"		/dev_stage="Adult"		/lab_host="DH10B (Life Technologies)"		/clone_lib="NCI CGAP ED1"		/note="Organ: Left Pubic Bone; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP ED1 is a normalized CDNA library containing the following tissue(s): Chondrosarcoma cell line CSS. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.		TAG_TISSUE=chondrosarcoma		TAG_LIB=UI-H-ED1		TAG_SEQ=CGTCAAGGCT"		ORIGIN		Query Match 68.5%; Score 648.4; DB 5; Length 662;		Best Local Similarity 99.4%; Pred. No. 5.8e-162;		Matches 649; Conservative 1; Mismatches 3; Indels 0; Gaps 0;		QY 268		GAAAAATACCAACAGAAAACCAAAACCAAAAGTCTGACATTTCTGAAAGATCTCTCTAGTGA		327		Db 662		GAAAAATACCAACAGAAAACCAAAACCAAAAGTCTGACATCTGAAAGATCTCTCTAGTGA		603		QY 328		AGCAAAACAGCATACAGTCTGCAAAATGCTACAAAGAACCCAGCGGAAACAAATTCACACCTC		387		Db 602		AGCAAAACAGCATACAGTCTGCAAAATGCTACAAAGAACCCAGCGGAAACAAATTCACACCTC		543		QY 388		AAGGCCCCCGCTGAAAAACCGTGACAGGACCTGCAACAGGCTGGCAGTAACTGTGCGG		447		Db 542		AAGGCCCCCGCTGAAAAACCGTGACAGGACCTGCAACAGGCTGGCAGTAACTGTGCGG		483		QY 448		CAACGTCACCGTCATTATCAGAGCTTTTAAGGAAAAGACTTCGCTCCTCATCGACATCTCTC		507		Db 482		CAACGTCACCGTCATTATCAGAGCTTTTAAGGAAAAGACTTCGCTCCTCATCGACATCTCTC		423		QY 508		ATCCACAGTGCACCTCCAGTGCAGGGTTCAGAACAGCAGAACCCAGAGCAGCTCCGGGTGAGA		567		Db 422		ATCCACAGTGCACCTCCAGTGCAGGGTTCAGAACAGCAGAACCCAGAGCAGCTCCGGGTGAGA		363		QY 568		GAGCACAGACAAGGGCTCTCCCGTCTCTCCACGCCAAAGGGCGACATGTGACAGTCAA		627		Db 362		GAGCACAGACAAGGGCTCTCCCGTCTCTCCACGCCAAAGGGCGACATGTGACAGTCAA		303		QY 628		TGATGAATCTTTCTGAAATTTGCACATGGAATTTGTGAAAACCTATGAATCAGGGTATGAAT		687	
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Db 302 TGATGATCTTTCTGAATTCACATGGAATTTGAAACTATGAATCAGGGTATGAAT 243
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Qy 748 CTCTTAGTAGTGTCCAGAGATAATTTCTGCTTGGCATGGCATCTGGCCACCAAGAAAT 807
Db 182 CTCTTAGTAGTGTCCAGAGATAATTTCTGCTTGGCATGGCATCTGGCCACCAAGAAAT 123
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Qy 868 CTAACAATCATTTATATAATTCGATGTGCTCTCGAATCTACTTTTATATAAAAAA 920
Db 62 CTAACAATCATTTATATAATTCGATGTGCTCTCGAATCTACTTTTATATAAAAAA 10

RESULT 9
CK299391/c
LOCUS
DEFINITION
  UI-E-EJ1-ajv-e-08-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
  UI-E-EJ1-ajv-e-08-0-UI 3', mRNA sequence.
ACCESSION
  CK299391
VERSION
  CK299391.1 GI:39887700
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 664)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  8889548
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Dr. Greg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/eye.html
  The following repetitive elements were found in this cDNA
  sequence: 1-23, >AT rich#Low_complexity
  Seq primer: M13 FORWARD
  POLYA=Yes.

FEATURES
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    Choroid"
    /dev_stage="fetal and adult"
    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
    /clone_lib="UI-E-EJ1"
    /notes="Organ: eye; Vector: pTT3-Pac (Pharmacia) with a
    modified polylinker; Site 1: EcoR I; Site 2: Not I;
    UI-E-EJ1 is a subtracted cDNA library constructed
    according to Bonaldo, Lennon and Soares, Genome Research,
    6:791-806, 1996. First strand cDNA synthesis was primed
    with an oligo-dT primer containing a Not I site. Double
```

```
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pTT3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dr)18 tail. The
sequence tags for this library are: fetal eyes,
AGATCAAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACTTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
TAG_ISSUE=human fetal eyes
TAG_LIB=UI-E-EJ1
TAG_SEQ=AGAATCAAGA"

ORIGIN
Query Match 67.3%; Score 637.2; DB 7; Length 664;
Best Local Similarity 99.2%; Pred. No. 5.7e-159;
Matches 639; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 277 CAACAGAAAAACCAACCAAGTGTGACATTTCTGAAGATCTCTCTAGTGAAGCAACAG 336
Db 653 CGAGGAGAAAAACCAACCAAGTGTGACATTTCTGAAGATCTCTCTAGTGAAGCAACAG 594
Qy 337 CATACAGTCTGCAATGCTTACAACAGACCGAGCAAAATCAACCTCAAGGCCCG 396
Db 593 CATACAGTCTGCAATGCTTACAACAGACCGAGCAAAATCAACCTCAAGGCCCG 534
Qy 397 GCTGAAAAACGTGACAGGAGCACTGCACAGCAGTTGGCAGTAACCTGGGCAACCTCAC 456
Db 533 GCTGAAAAACGTGACAGGAGCACTGCACAGCAGTTGGCAGTAACCTGGGCAACCTCAC 474
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Qy 517 GACCTCCAGTGCAGGTCAGAACAGCAGAACAGACAGCTCGGGTTCAGAGGACACAGA 576
Db 413 GACCTCCAGTGCAGGTCAGAACAGCAGAACAGACAGCTCGGGTTCAGAGGACACAGA 354
Qy 577 CAAGGCTCTCTCCCGTTCTCTCCACGCAAGGCGCACATGTGAGCAGTCAATGATGAATC 636
Db 353 CAAGGCTCTCTCCCGTTCTCTCCACGCAAGGCGCACATGTGAGCAGTCAATGATGAATC 294
Qy 637 TTTCTGAAATTCACATGGAATTTTGAAACTATGAAATCAGGGTATGAAATTCAAAACCT 696
Db 293 TTTCTGAAATTCACATGGAATTTTGAAACTATGAAATCAGGGTATGAAATTCAAAACCT 234
Qy 697 CCACCTGCCCATGCTGTCATCCCTGAGAAATCTTCTGTGACATCGACATCGACCTTTAGTG 756
Db 233 CCACCTGCCCATGCTGTCATCCCTGAGAAATCTTCTGTGACATCGACCTTTAGTG 174
Qy 757 ATGCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAGGAATTTTCGACCC 816
Db 173 ATGCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAGGAATTTTCGACCC 114
Qy 817 TGAAGATTAATCTTGTACACTTTTATGATATTCATGTTTATATGATTTTCTTAAACATC 876
Db 113 TGAAGATTAATCTTGTACACTTTTATGATATTCATGTTTATATGATTTTCTTAAACATC 54
Qy 877 ATTATAATTCGATGTGCTCTGAAATCTACTTTTATATAAAAAA 920
Db 53 ATTATAATTCGATGTGCTCTGAAATCTACTTTTATATAAAAAA 10

RESULT 10
BQ189224
LOCUS
DEFINITION
  UI-E-EJ1-ajv-e-08-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
  UI-E-EJ1-ajv-e-08-0-UI 5', mRNA sequence.
ACCESSION
  BQ189224
VERSION
  BQ189224.1 GI:20364775
KEYWORDS
  EST.
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SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 650)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road,
 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.reagen.com).
 The following repetitive elements were found in this CDNA
 sequence: 626-650, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 REVERSE
 Location/Qualifiers
 1. 650
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-EJ1-ajv-e-08-0-UI"
 /tissue_type="fetal eyes, lens, eye anterior segment,
 optic nerve, retina, Retina Foveal and Macular, RPE and
 Choroid"
 /dev_stage="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-EJ1"
 /note="Organ: eye; Vector: pTT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-EJ1 is a subtracted CDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pTT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are: fetal eyes,
 AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
 AATCCGCAT; optic nerve, CCATTAGGTG; retina, CCGCG; Retina
 Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
 library was created for the program, Gene Discovery in the
 Visual System, supported by National Eye Institute (NEI)."

Query Match 66.7%; Score 631.2; DB 5; Length 650;
 Best Local Similarity 99.1%; Pred. No. 2.3e-157;
 Matches 633; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 282 AGAAACCAACCAAGTCTGACATTCCTGAAGATCTCTCTAGTGAAGCAAGCATAC 341
 DB 1 AGAAACCAACCAAGTCTGACATTCCTGAAGATCTCTCTAGTGAAGCAAGCATAC 60
 QY 342 AGTCTGCAATGCTACCAAGACCGGCAACAAATCACCTCAAGGCCCGGCTGA 401
 DB 61 AGTCTGCAATGCTACCAAGACCGGCAACAAATCACCTCAAGGCCCGGCTGA 120
 QY 402 AAAACGTGGACAGGAGCTGCACAGCAGTGTGGCAGTAACCTGTGGCAACCTCACCGTCA 461
 DB 121 AAAACGTGGACAGGAGCTGCACAGCAGTGTGGCAGTAACCTGTGGCAACCTCACCGTCA 180

462 TTATCAGACAGCTTTAAGGAAAAGACTCGCTCTCTCATCGACATCTCTCATCCACAGTGCCT 521
 181 TTATCAGACAGCTTTAAGGAAAAGACTCGCTCTCTCATCGACATCTCTCATCCACAGTGCCT 240
 QY 522 CAGTGCAGGCTCAGAAACAGCAGCAACAGCAGCTCGGGTTCAGAGCAGCAGACAAGG 581
 DB 241 CCAGTGCAGGCTCAGAAACAGCAGCAACAGCAGCTCGGGTTCAGAGCAGCAGACAAGG 300
 QY 582 GCTCTCCCGTTCTCCACGCCAAAGGGCGACATGTGACAGTCAATGATGAATCTTTCT 641
 301 GCTCTCCCGTTCTCCACGCCAAAGGGCGACATGTGACAGTCAATGATGAATCTTTCT 360
 QY 642 GAAATTCACATGGAATTGTGAAACTATGAATCAGGGTATGAAATTCAAAACCTCCACC 701
 DB 361 GAAATTCACATGGAATTGTGAAACTATGAATCAGGGTATGAAATTCAAAACCTCCACC 420
 QY 702 TGCCCATGCTGTGTCATCCCTGGAGAACTTCTGTGGACATCGACTCTTACTGATGCT 761
 DB 421 TGCCCATGCTGTGTCATCCCTGGAGAACTTCTGTGGACATCGACTCTTACTGATGCT 480
 QY 762 GCCAGATTAATTTCTGCTTGCCATGGCATCTGCCACCAAGGAATTTCCACCTGACG 821
 DB 481 GCCAGATTAATTTCTGCTTGCCATGGCATCTGCCACCAAGGAATTTCCACCTGACG 540
 QY 822 ATTACTCTTGACACTTTTATGTATTCATTTGTTTATATGATTTCTTAACTCATTTA 881
 DB 541 ATNACTCTTGACACTTTTATGTATTCATTTGTTTATATGATTTCTTAACTCATTTA 600
 QY 882 TAATTGGATGTGCTCTCGAATCTACTTTTATATAAAAAA 920
 DB 601 TAATTGGATGTGCTCTCGAATCTACTTTTATATAAAAAA 639

RESULT 11
 BF116048/c
 LOCUS
 DEFINITION
 FACTOR: mRNA sequence.
 BF116048
 EST.
 BF116048.1 GI:10985524
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 642)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-xemail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento
 Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 457.
 Location/Qualifiers
 1. 642
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3570638"
 /tissue_type="fibrotheoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NCI_CGAP_Ov18"

FEATURES
 source

/note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st TGTACCAATCTGAAGTGGAGGCGCGGACATTTTCTTTTCTTTT 3'; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN		Query Match	65.2%; Score 617.6; DB 2; Length 642;
		Best Local Similarity	98.9%; Pred. No. 9.9e-154;
		Matches	631; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
Qy	277 CAACAAGAAACCAACCAAG-TCTGACATTTCTGAAGATCTCTTCTAGTGAAGCAACA	335	
Db	638 CCACAAGAAACCCGAACCAAGTTCTGACATTTTGAAGATCTCTTCTAGTGAAGCAACA	579	
Qy	336 GCATACAGTCTGCAATGCTTACACAAAGACCGGAAACAAATCACACCTCAAGGCCCC	395	
Db	578 GCATACAGTCTGCAATGCTTACACAAAGACCGGAAACAAATCACACCTCAAGGCCCC	519	
Qy	396 GGCTGAAACCGTGGACAGGACCTGCACAGCAGTTGGCAGTAACTGTGGCAACGTCA	455	
Db	518 GGCTGAAACCGTGGACAGGACCTGCACAGCAGTTGGCAGTAACTGTGGCAACGTCA	459	
Qy	456 CCGTCATTATCACAGATTTAAGGAAAGACTCGCTCTCATCGACATCTTCATCCACAG	515	
Db	458 CCGTCATTATCACAGATTTAAGGAAAGACTCGCTCTCATCGACATCTTCATCCACAG	399	
Qy	516 TGACCTCCAGTGCAGGCTCAGACAGCAGACCAAGCAGCTCGGGTTCAGAGGACAG	575	
Db	398 TGACCTCCAGTGCAGGCTCAGACAGCAGACCAAGCAGCTCGGGTTCAGAGGACAG	339	
Qy	576 ACAAGGGCTCTCCCGTTCTCCACGCAAGGGCGACATGTGACAGTCAATGATGAAT	635	
Db	338 ACAAGGGCTCTCCCGTTCTCCACGCAAGGGCGACATGTGACAGTCAATGATGAAT	279	
Qy	636 CTTTCTGAAATTCGACATGGAATTTGAAACTATGATCAGGATGAAATTCAAACCC	695	
Db	278 CTTTCTGAAATTCGACATGGAATTTGAAACTATGATCAGGATGAAATTCAAACCC	219	
Qy	696 TCACCTGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	755	
Db	218 TCACCTGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	159	
Qy	756 GATGCTGCCAGGATAATTTCTGCTTGGCATGGGCACTCTGGCCACCAAGGAATTCGCACC	815	
Db	158 GATGCTGCCAGGATAATTTCTGCTTGGCATGGGCACTCTGGCCACCAAGGAATTCGCACC	99	
Qy	816 CTGACGATTAATCTTGACATTTTATGATATTCATGTTTATGATATTTCTTAAACAT	875	
Db	98 CTGACGATTAATCTTGACATTTTATGATATTCATGTTTATGATATTTCTTAAACAT	39	
Qy	876 CATTTATAATGGATGGCTCCCTGAAATCTACTTTTAT 913		
Db	38 CATTTATAATGGATGGCTCCCTGAAATCTACTTTTAT 1		

RESULT 12
AI627241/c
LOCUS
DEFINITION ty72411.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2284604 3', similar to TR:Q99710 Q99710 YY1-ASSOCIATED FACTOR 2. ;, mRNA
sequence.
ACCESSION AI627241
VERSION AI627241.1 GI:4664041
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

4/23/99

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 621)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio-llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 463.

FEATURES
source

1..621
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2284604"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

		Query Match	64.8%; Score 613.2; DB 1; Length 621;
		Best Local Similarity	99.0%; Pred. No. 1.5e-152;
		Matches	615; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy	293 CCAAGTCTGACATTTCTGAAGATCTCTCTAGTGAAGCAACAGCATACAGTCTGCAAT	352	
Db	621 CCAAGTCTGACATTTCTGAAGATCTCTCTAGTGAAGCAACAGCATACAGTCTGCAAT	562	
Qy	353 GTTACAAACAAAGACGAGCAAAATCACTCAAGGCCCCGGCTGAAAACCTGGAC	412	
Db	561 GCTACAAACAAAGACGAGCAAAATCACTCAAGGCCCCGGCTGAAAACCTGGAC	502	
Qy	413 AGGAGCAGTGCACAGCAGTGGCAGTAACTGTGGGCAAGCTCACCGTCAATTCACAGAC	472	
Db	501 AGGAGCAGTGCACAGCAGTGGCAGTAACTGTGGGCAAGCTCACCGTCAATTCACAGAC	442	
Qy	473 TTTAAGAAAAGACTCGCTCTCATCGACATCTCTATCCACAGTACCTCCAGTGCAGGG	532	
Db	441 TTTAAGAAAAGACTCGCTCTCATCGACATCTCTATCCACAGTACCTCCAGTGCAGGG	392	
Qy	533 TCAGAACAGCAGAACCCAGAGCAGCTCGGGTTCAGAGAGCAGACAGAGGGCTCTCCCGT	592	
Db	381 TCAGAACAGCAGAACCCAGAGCAGCTCGGGTTCAGAGAGCAGACAGAGGGCTCTCCCGT	322	
Qy	593 TCTCCACGCCAAAGGGCGACATGTCCAGCTCAATGATGAATCTTCTGAAATTCGACA	652	
Db	321 TCTCCACGCCAAAGGGCGACATGTCCAGCTCAATGATGAATCTTCTGAAATTCGACA	262	
Qy	653 TGGAAATTTGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTG	712	
Db	261 TGGAAATTTGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTG	202	
Qy	713 CTTGCAATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAAT	772	
Db	201 CTTGCAATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAAT	142	

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773 TTCTGCTTGCATGGGCACTGGCCACCAAGGAATTCGCACCTGACGATTAATCTTGA 832
Db      |||||
141 TTCTGCTTGCATGGGCACTGGCCACCAAGGAATTCGCACCTGACGATTAATCTTGA 82
Qy      |||||
833 CACTTTATGATTCGATTTGTTTATGATTTTCTTAAACAATCATTATTAATGGATGT 892
Db      |||||
81 CACTTTATGATTCGATTTGTTTATGATTTTCTTAAACAATCATTATTAATGGATGT 22
Qy      |||||
893 GCTCTCGAATCTACTTTTAT 913
Db      |||||
21 GCTCCTGAATCTACATTTTAT 1

RESULT 13
CN533672
LOCUS      792 bp mRNA linear EST 29-APR-2004
DEFINITION UI-M-HO0-cp2-g-18-0-UI.r1 NIH BMAP_HO0 Mus musculus cDNA clone
CN533672
IMAGE:30655169 5', mRNA sequence.
ACCESSION CN533672
VERSION    1
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE
1 (bases 1 to 792)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Dr. James Lin University of Iowa
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Distribution information can be found at
          http://genome.uiowa.edu/distribution/mousefl.html
          This clone was contributed by the Brain Molecular Anatomy Project
          (BMAP)

The following repetitive elements were found in this cDNA
sequence: 708-733, >AT_rich#Low_complexity
Seq primer: pYX-5.

FEATURES             source
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     /organism="Mus musculus"
     /mol_type="mRNA"
     /strain="C57BL/6"
     /db_xref="taxon:10090"
     /clone="IMAGE:30655169"
     /tissue_type="Upper Head"
     /dev_stage="9.5-10.5 dpc"
     /lab_host="DH10B (TI phage resistant)"
     /clone_lib="NIH BMAP_HO0"
     /note="Organ: Head; Vector: pYX-Asc; Site 1: Ecor I;
     Site 2: Not I; The library was constructed according
     Bonaïdo, Lennon and Soares, Genome Research, 6:791-806,
     1996. Denatured RNA was size fractionated on a 1% agarose
     gel. First strand cDNA synthesis was primed with oligo-dT
     primer containing a Not I site. Double strand cDNA was
     size selected according to mRNA size fraction, ligated
     with Ecor I adaptor, digested with NotI and then cloned
     directionally into pYX-Asc vector. The library tag
     sequence located between the Not I site and the polyA tail
     is CGAATGGAAT. This library was created for the University
     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
     Developing Mouse Nervous System', supported by National
     Institute of Mental Health (NIMH)."
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ORIGIN

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Query Match      64.1%; Score 607.2; DB 7; Length 792;
Best Local Similarity 92.4%; Pred. No. 6.3e-151;
Matches 671; Conservative 1; Mismatches 49; Indels 5; Gaps 3;
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195 AGAAGGAGAAAGTTGAAAAGCAGGACCAAGAGAAACCTCAGAAAGACCAAGGAATTAATGTC 254
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1 AGAAGGAGAAAGTTGAAAAGCCTCGAAAAGCCCTGCAAAAGAAAAGCCAGAGAAAGCAAGGCAATAGCC 60
Qy      |||||
255 CTAGTGTACCAAGAAAATACCAACAGAAAACCAAAAGTCTGACATTCCTGAAG 314
Db      |||||
61 CCAGTGTACCAAGAAAACACCAACAGAAAACCAAAAGTCTGATATTTCTGAAG 120
Qy      |||||
315 ATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACCAAGGAAA 374
Db      |||||
121 ATCTCTCTAGTGAAGCTTAACAGCATACAGTCTGCTAAACGCTACCAACAAAGACCAAGGAAA 180
Qy      |||||
375 CAAATCACACCTCAAGGCCCGGCTGAAAACCTGAGACAGGAGCATGTCAGCAGCTGG 434
Db      |||||
181 CAAACCAACCTCAAGGCCCGGCTGAAGAATGTGACAGGAGCACCGCAGCAGCTGG 240
Qy      |||||
435 CAGTAACTGTGGGACAGTCACCGTCAATATACAGACTTTAAGGAAAAGACTCGCTCCT 494
Db      |||||
241 CAGTAACTGTGGGCAACGTCACCGTCAATATACAGACTTTAAGGAAAAGACTCGCTCCT 300
Qy      |||||
495 CATCGACATCCTCATCCACAGTGACCTCCAGTGCAGGGTCCAGAACAGCAGAGAACAGASCA 554
Db      |||||
301 CTCCACATCCTCTTCCACAGTGACCTCCAGTGCAGGGTCCAGAACAGCAGAGAACAGAGCA 360
Qy      |||||
555 GTCGGGGTTCAGAGACACAGACAGAGGGCTCTCCCGTCTCCACGCCCAAGGGGAGCA 614
Db      |||||
361 GCTCGGGCTCAGAGACACAGACAGAGGGCTCTCCCGCTCTCCACGCCCAAGGGGAGCA 420
Qy      |||||
615 TGTACAGCTCAATGATGATCTTTCTGAAATGACATGGAATTTGAAACATATGAAT 674
Db      |||||
421 TGTACAGCTCAATGATGATCTTTCTGAAATGACATGGAATTTG-ANAATATGAAT 479
Qy      |||||
675 CAGGCTATGAAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCCCTGGAGAATCTTC 734
Db      |||||
480 CAGGCTATGAGATTCAAAACCTCCACCTGCCATGCTGCTTGA-CCCTGGAGAGTCTTC 538
Qy      |||||
735 TGTGGACATGACCTCTTAGTGTAGTGCAGAGATAATTTCTGCTGCCATGGGACATCTG 794
Db      |||||
539 TGTGGA---CGACCTTGATTGACGCTACCCAGGAGAGGTTCCGCTTGGCGGACATCTG 595
Qy      |||||
795 GCACCAAGGAATTTCCGACCTCGACGATTAATCTTGCACACTTTTATGATTTCAATGTT 854
Db      |||||
596 GCTACCAAGGAATTTCTGACCTTGCAGTACTCTTGACACTTTTATGATTTCAATGTT 655
Qy      |||||
855 TTATATGATTTTCTTAACAATCATTATTAATTTGATGCTCTCTGATCTTACTTTTATA 914
Db      |||||
656 TTATATGATTTTCTTAACAATCATTATTAATTTGATGCTCTCTGATCTTACTTTTATA 715
Qy      |||||
915 AAAAAA 920
Db      |||||
716 TATATA 721

RESULT 14
CN534466
LOCUS      784 bp mRNA linear EST 28-JAN-2004
DEFINITION UI-M-HN0-cnl-o-13-0-UI.r1 NIH BMAP_HN0 Mus musculus cDNA clone
CN534466
IMAGE:30643452 5', mRNA sequence.
ACCESSION CN534466
VERSION    1
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE
1 (bases 1 to 784)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Dr. James Lin University of Iowa
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
```

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution Information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

The following repetitive elements were found in this cDNA

sequence: 704-729, >AT_rich#Low_complexity
Seq primer: pYX-5.

FEATURES

Location/Qualifiers

1. .784
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30643452"
/tissue_type="Upper Head"
/dev_stage="9.5-10.5 dpc"
/lab_hosts="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HNO"

/notes="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAATCTGAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 63.9%; Score 604.8; DB 7; Length 784;
Best Local Similarity 92.5%; Pred. No. 2.7e-150;
Matches 668; Conservative 1; Mismatches 48; Indels 5; Gaps 3;
QY 199 GGAGAAAGTTGAAAGCAGGACAAAGAGAAACCTGTGAAAGAGACAAAGGAAATTAGTCTCTAG 258
DB 1 GGAGAAAGTCTGAAAGCCTGACAAAGAAAGAAAGCCAGAGAAAGACAAAGACATTAGGCCCCAG 60
QY 259 TGTACCAAGAAATATCCAAACAGAAACAAACAAAGTCTGACATTCCTGAAAGATCC 318
DB 61 TGTACCAAGAAATATCCAAACAGAAACAAACAAAGTCTGATATCTGAAAGATCC 120
QY 319 TCCTAGTGAAGCAACACAGCATACAGTCTGCAATGTCTACAAAGACCAAGACCAAGAAACAA 378
DB 121 TCCTAGTGAAGCTAACAGCATACAGTCTGTACGCTTACAAAGACCAAGACCAAGAAACAA 180
QY 379 TCACACCTCAAGGCCCGGCTGAAAGAAACGTGGACAGGAGCACTGACACAGCAGTTGGCAGT 438
DB 181 CCACACCTCAAGGCCCGGCTGAAAGATGTGGACAGGACACCGCACAGCAGTTGGCAGT 240
QY 439 AACTGTGGGCAACGTACCGCTCATATACAGACTTTAAGAAAGAACTGCTCCTCATC 498
DB 241 AACTGTGGGCAACGTACCGCTCATATACAGACTTTAAGAAAGAACTGCTCCTCATC 300
QY 499 GACATCTCTATCCACAGTGAACCTCCAGTGCAGGCTCAGAAACAGACAGACCAAGACCAAGACCTC 558
DB 301 CACATCTCTTCCAGATGACCTCCAGTGCAGGCTCAGAAACAGACAGACCAAGACCAAGACCTC 360
QY 559 GGGGTACAGAGACACAGAGGGCTCCTCCCGTTCTCTCCAGCGCAAGAGGGCGGACATGTC 618
DB 361 GGGGTACAGAGACACAGAGGGCTCCTCCCGTTCTCTCCAGCGCAAGAGGGCGGACATGTC 420
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AY400131
LOCUS
DEFINITION
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genomic survey sequence.
ACCESSION
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VERSION
AY400131.1
KEYWORDS
GSS.
SOURCE
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ORGANISM
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
REFERENCE
2 (bases 1 to 654)
AUTHORS
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment
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ORIGIN
Query Match 62.6%; Score 593; DB 9; Length 654;
Best Local Similarity 97.1%; Pred. No. 3.7e-147;
Matches 602; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1019.4	90.1	1036	21	US-10-956-157-1792
3	1019.4	90.1	1036	21	US-10-956-157-7027
4	1019.4	90.1	1128	21	US-10-489-740-35
5	935.8	82.7	1128	14	US-10-103-313-121
6	468.4	41.4	502	10	US-09-918-995-24859
7	436	38.5	719	9	US-09-764-848-12

8	436	38.5	719	14	US-10-116-016-12	Sequence 12, Appl
9	436	38.5	719	14	US-10-103-313-247	Sequence 247, App
10	436	38.5	719	16	US-10-222-020-12	Sequence 12, Appl
c 11	427.4	37.8	429	9	US-09-864-761-4575	Sequence 4575, Ap
c 12	337.4	29.8	467	21	US-10-505-680-571	Sequence 571, App
c 13	316.6	28.0	400	21	US-10-505-680-570	Sequence 570, App
c 14	285.6	25.3	326	17	US-10-242-783A-10941	Sequence 10941, A
c 15	285.6	25.3	326	18	US-10-085-783A-10941	Sequence 10941, A
c 16	232.8	20.6	253	9	US-09-864-761-21320	Sequence 21320, A
c 17	168.4	14.9	470	9	US-09-864-761-10204	Sequence 10204, A
c 18	159.4	14.1	1033	9	US-09-954-531-582	Sequence 582, App
c 19	159.4	14.1	1033	21	US-10-843-641A-1649	Sequence 1649, Ap
c 20	156.6	13.8	466	10	US-09-918-995-22728	Sequence 22728, A
c 21	154.2	13.6	799	21	US-10-956-157-4587	Sequence 4587, Ap
c 22	139.8	12.4	430	20	US-10-357-930-54267	Sequence 54267, A
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c 28	75	6.6	75	9	US-09-864-761-26844	Sequence 26844, A
c 29	73	6.5	231	21	US-10-877-320-20	Sequence 20, Appl
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c 31	65.2	5.8	714	20	US-10-363-345A-15101	Sequence 15101, A
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c 34	65.2	5.8	714	21	US-10-363-483A-15102	Sequence 15102, A
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c 41	56.8	5.0	288	15	US-10-279-964-29	Sequence 29, Appl
c 42	55.2	4.9	474	16	US-10-314-669-142	Sequence 142, App
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c 44	55.2	4.9	2839	14	US-10-125-237-89	Sequence 89, Appl
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ALIGNMENTS

RESULT 1

US-10-505-680-569
; Sequence 569, Application US/10505680
; Publication No. US2005009592A1

GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.
; APPLICANT: Boyd, Jeff

; APPLICANT: Liu, Edison T.

; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TA

; FILE REFERENCE: 4239-64452

; CURRENT APPLICATION NUMBER: US/10/505,680

; CURRENT FILING DATE: 2004-08-12

; PRIOR APPLICATION NUMBER: 60/357,031

; PRIOR FILING DATE: 2002-02-13

; NUMBER OF SEQ ID NOS: 822

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 569

; LENGTH: 1036

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-505-680-569

Query Match 90.1%; Score 1019.4; DB 21; Length 1036;

Best Local Similarity 99.4%; Pred. No. 2.9e-292;

Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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; Sequence 1792, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1792
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-1792

Query Match 90.1%; Score 1019.4; DB 21; Length 1036;
Best Local Similarity 99.4%; Pred. No. 2.9e-292;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 75 CCACGAGAGCGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGTACAG 134
Db 1 CCCGGACGGCGTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGTACAG 60
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DB 1021 TAATAAAAA 1029
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; Sequence 7027, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7027
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-7027

Query Match 90.1%; Score 1019.4; DB 21; Length 1036;
Best Local Similarity 99.4%; Pred. No. 2.9e-292;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 75 CCACGAAGGCCTTTCTCTCCGAGCGCGCCGCTTTTCGGCTTGGGGGGGGGGGTACAG 134
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QY 975 ATCTGGCCACCAAGAAATTCGACCCCTGACGATTAATTTGACACTTTTATGATTTCCA 1034
DB 901 ATCTGGCCACCAAGAAATTCGACCCCTGACGATTAATTTGACACTTTTATGATTTCCA 960
QY 1035 TTGTTTTATATGATTTTCTTAACAATCATTTATAATTTGATGTGCTCTGATCTACTTT 1094
DB 961 TTGTTTTATATGATTTTCTTAACAATCATTTATAATTTGATGTGCTCTGATCTACTTT 1020
QY 1095 TTATAAAAA 1103
DB 1021 TAATAAAAA 1029
RESULT 4
US-10-489-740-35
; Sequence 35, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: P9
; FILE REFERENCE: Angiogenesis_PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-740-35
Query Match 90.1%; Score 1019.4; DB 21; Length 1128;
Best Local Similarity 99.4%; Pred. No. 3.1e-292;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 75 CCACGAAGGCCTTTCTCTCCGAGCGCGCCGCTTTTCGGCTTGGGGGGGGGGGTACAG 134
DB 85 CCGGACGGGTTTCTCTCCGAGCGCGCGCTTTTCGGCTTGGGGGGGGGGGTACAG 144
QY 135 CCATCCATGACATCGGCGGACAGAGAGCCGACGAGCCCAAAAGACAGCGAAACC 194

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145 CCCATCATGACCATGGCGCAAGAGAGCCGACAGGCGCAAAAGACAAAGCGAAACC 204
195 TGCCGACAGAAAGGGTTTGGGATTGAGCGTTGACACCTTGCAGAAACAGTGTGTAAGC 254
205 TGCCGACAGAAAGGGTTTGGGATTGAGCGTTGACACCTTGCAGAAACAGTGTGTAAGC 264
255 CTTTAAATGACGATCTCGGATGTGAGGAAAGGACCTCCACGAGAAACCTCGGATCAA 314
265 CTTTAAATGACGATCTCGGATGTGAGGAAAGGACCTCCACGAGAAACCTCGGATCAA 324
315 TTCTCAGCTGTGGCACAACAAGTGGCAACAGTATGCCACCCACACCCCTCAAAAA 374
325 TTCTCAGCTGTGGCGCAACAAGTGGCAACAGTATGCCACCCACACCCCTCAAAA 384
375 GGAGAAAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAAT 434
385 GGAGAAAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAAT 444
435 TAGTCTTAGTGTACCAAGAAATATCCAAAGAAACCAAAACCAAAAGTGTGACATTCT 494
445 TAGTCTTAGTGTACCAAGAAATATCCAAAGAAACCAAAACCAAAAGTGTGACATTCT 504
495 GAAAGATCCTCTTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAACAAAGACGAG 554
505 GAAAGATCCTCTTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAACAAAGACGAG 564
555 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACCGTGACAGGAGCACTGCACAGCA 614
565 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACCGTGACAGGAGCACTGCACAGCA 624
615 GTTGGCAGTAACTGTGGGCAAGCTCACCGTCAATTATCACAGACTTAAAGGAAAGACTCG 674
625 GTTGGCAGTAACTGTGGGCAAGCTCACCGTCAATTATCACAGACTTAAAGGAAAGACTCG 684
675 CTCTCTATCGACATCTCTCATCACAGTGACCTCAGTGCAGGGTCAGAAACAGCAGAAACCA 734
685 CTCTCTATCGACATCTCTCATCACAGTGACCTCAGTGCAGGGTCAGAAACAGCAGAAACCA 744
735 GAGCAGCTCGGGGTGAGAGACACAGCAAGGGGCTCTCCGTTCTCCACGCGCAAGGG 794
745 GAGCAGCTCGGGGTGAGAGACACAGCAAGGGGCTCTCCGTTCTCCACGCGCAAGGG 804
795 CGACATGTCAGCAGTCAATGATGATCTTTTGTGAAATGACATGGAATTTGTGAAACTA 854
805 CGACATGTCAGCAGTCAATGATGATCTTTTGTGAAATGACATGGAATTTGTGAAACTA 864
855 TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCGCATGCTGTGATCCCTGGAGAA 914
865 TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCGCATGCTGTGATCCCTGGAGAA 924
915 TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGC 974
925 TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGC 984
975 ATCTGGCCACCAAGGAATTTGGCACCCTGACGATTAATTTGACACTTTTATGTTATCCA 1034
985 ATCTGGCCACCAAGGAATTTGGCACCCTGACGATTAATTTGACACTTTTATGTTATCCA 1044
1035 TTGTTTTATATGATTTTCTTAACCAATCATTTATATTTGGAATGCTCTGAAATCTACTTT 1094
1045 TTGTTTTATATGATTTTCTTAACCAATCATTTATATTTGGAATGCTCTGAAATCTACTTT 1104
1095 TTATAAAAA 1103
1105 TTATAAAAA 1113
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RESULT 5
US-10-103-313-121
; Sequence 121, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-103-313-121

Query Match      82.7%; Score 935.8; DB 14; Length 2156;
Best Local Similarity 99.2%; Pred. No. 3.6e-267;
Matches 951; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

146 CCATGGCGCAACAAGAGAGCCCGACAGGCGCAAAAGACAAAGCGAAACCTGCCGACAGC 205
1 CCAGCGGTCCGAAGAGAGAGCCCGACAGGCGCAAAAGACAAAGCGAAACCTGCCGACAGC 60
206 AAGGGTTTTTGGGATTGTAGCGTCTGCACCTTTCAGAAAACAGTGTGTAAGCCTTTAAATGCA 265
61 AAGGGTTTTTGGGATTGTAGCGTCTGCACCTTTCAGAAAACAGTGTGTAAGCCTTTAAATGCA 120
266 GCATCTCGGATGTGAGGAAAGGACCTCCACCA- GAAAACCTCGGATCAATTTCTCAGCTG 324
121 GCATCTCGGATGTGAGGAAAGGACCTCCACCAAGTATGCCACCCACCCCTTAAAGAGAG 180
325 GTGSCACAACAAGTGGCACAACAGTATGCCACCCACCCACCCCTTAAAGAGAGAGAAAG 384
181 GTGSCACAACAAGTGGCACAACAGTATGCCACCCACCCACCCCTTAAAGAGAGAGAAAG 240
385 GAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAAGCAAGGAAAATTAGTCTTAGT 444
241 GAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAAGCAAGGAAAATTAGTCTTAGT 300
445 GTTACCAAGAAAATACCAACAAGAAAACCAACCAAGTGTGACATTTCTGAAAGATCCT 504
301 GTTACCAAGAAAATACCAACAAGAAAACCAACCAAGTGTGACATTTCTGAAAGATCCT 360
505 CCTAGTGAACCAACAGCATACTAGTCTGCAAAATGCTACAACAAAGACACAGCGAAAACAAAT 564
361 CCTAGTGAACCAACAGCATACTAGTCTGCAAAATGCTACAACAAAGACACAGCGAAAACAAAT 420
565 CACACCTCAAGGGCCCGGCTGAAAAACGTCGACAGGAGCACTGCACAGCAGTTGGCAGTA 624
421 CACACCTCAAGGGCCCGGCTGAAAAACGTCGACAGGAGCACTGCACAGCAGTTGGCAGTA 480
625 ACTGTGGGCAACGTCACCGTCATTATCAGACCTTTAAGGAAAAGACTCGCTCTCATCG 684
481 ACTGTGGGCAACGTCACCGTCATTATCAGACCTTTAAGGAAAAGACTCGCTCTCATCG 540
685 ACATCTCTCATCCACAGTGACCTCCAGTCGAGGGTCAGAACAGACAGAACACAGAGCAGCTCG 744
541 ACATCTCTCATCCACAGTGACCTCCAGTCGAGGGTCAGAACAGACAGAACACAGAGCAGCTCG 600
745 GGGTCAGAGAGCAGACAGAAAGGGCTCTCCCGTTCTCCACGCGAAAAGGGCGACATGTCA 804
601 GGGTCAGAGAGCAGACAGAAAGGGCTCTCCCGTTCTCCACGCGAAAAGGGCGACATGTCA 660
805 GCAGTCAATGATGAATCTTTGTGAAATTCACATGGAATTTGTGAAAACCTATGAATCAGGG 864
661 GCAGTCAATGATGAATCTTTGTGAAATTCACATGGAATTTGTGAAAACCTATGAATCAGGG 720
865 TATGAAATTCAAAACCTCCACCTGCCCATGCTGTTCATCTCCCTGGAGAAATCTTCTGTGG 924
721 TATGAAATTCAAAACCTCCACCTGCCCATGCTGTTCATCTCCCTGGAGAAATCTTCTGTGG 780
925 ACATCGACCTCTTAGTGATGCTGCCAGGATAAATTTCTGCTTGCATGGGCAATCTGGCCAC 984
781 ACATCGACCTCTTAGTGATGCTGCCAGGATAAATTTCTGCTTGCATGGGCAATCTGGCCAC 840
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QY 985 CAAGGAATTTGGCACCCTGACGATTACTCTTGACACTTTTATGTATTCATTGTTTATA 1044
Db 841 CAAGGAATTTGGCACCCTGACGATTACTCTTGACACTTTTATGTATTCATTGTTTATA 900
QY 1045 TGATTTTCTCAACAATCAATTTATATATGATGTCTCTGAACTACTTTTATAAAAA 1103
Db 901 TGATTTTCTCAACAATCAATTTATATATGATGTCTCTGAACTACTTTTATAAAAA 959

RESULT 6

US-09-918-995-24859
; Sequence 24859, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24859
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(502)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-24859

Query Match 41.4%; Score 468.4; DB 10; Length 502;
Best Local Similarity 96.6%; Pred. No. 2.2e-128;
Matches 478; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 522 CATACAGTCTGAATGTCTAGCAAGACGAGCAAAATCAATCACTCAAGGCCCG 581
Db 8 CNAATAGATCGTATAGGCGCTCGAGGACCGAGCAAAATCACTCAAGGCCCG 67
QY 582 GCTGAAACGTTGGCAGGACACTGACAGCAGTTGGCAGTAATCTGTGGGCAAGCTAC 641
Db 68 GCTGAAACGTTGGCAGGACACTGACAGCAGTTGGCAGTAATCTGTGGGCAAGCTAC 127
QY 642 CGTCAATATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACATCTCATCCACAGT 701
Db 128 CGTCAATATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACATCTCATCCACAGT 187
QY 702 GACCTCCAGTGCAGGTTCAGAACAGCAGAACAGCAGCAGCTCGGGTCAGAGCAGACA 761
Db 188 GACCTCCAGTGCAGGTTCAGAACAGCAGAACAGCAGCAGCTCGGGTCAGAGCAGACA 247
QY 762 CAAGGCTCTCCCGTTCTCCACGCGCAAGGCGCAGATGTCAGCAGTCAATGATGATC 821
Db 248 CAAGGCTCTCCCGTTCTCCACGCGCAAGGCGCAGATGTCAGCAGTCAATGATGATC 307
QY 822 TTTGTGAATTCGACATGGAATTTGTGAAACTATGAATCAGGGTATGAAATTCAGAACT 881
Db 308 TTTGTGAATTCGACATGGAATTTGTGAAACTATGAATCAGGGTATGAAATTCAGAACT 367
QY 882 CCACCTGCCATGCTGCTTGCATCTCTGAGAAATCTTCTGTGGACATCGACCTCTTAGTG 941
Db 368 CCACCTGCCATGCTGCTTGCATCTCTGAGAAATCTTCTGTGGACATCGACCTCTTAGTG 427
QY 942 ATGCTGCCAGGATAATTTCTGCTTGGCCTGCGCATCTGCCACCAAGGAAATTCGACCC 1001
Db 428 ATGCTGCCAGGATAATTTCTGCTTGGCCTGCGCATCTGCCACCAAGGAAATTCGACCC 487
QY 1002 TGACGATTACTCTTG 1016

Db 488 TGACGATTACTCTTG 502

RESULT 7

US-09-764-848-12
; Sequence 12, Application US/09764848
; Patent No. US20020077270A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ08
; CURRENT APPLICATION NUMBER: US/09/764,848
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (621)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (626)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (643)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (658)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (712)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-848-12

Query Match 38.5%; Score 436; DB 9; Length 719;
Best Local Similarity 98.7%; Pred. No. 1.2e-118;
Matches 458; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 157 AAGAAGAGCCCGACCGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 216
Db 1 AAGAAGAGCCCGACCGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 60
QY 217 GATTGTAGCTGTGACCTTCAGAAACAGTCTGAGGCTTTAATGAGCATCTGCGAT 276
Db 61 GATTGTAGCTGTGACCTTCAGAAACAGTCTGAGGCTTTAATGAGCATCTGCGAT 120
QY 277 GTGAGGAAGGCACCTCCACAGCAAAACCTCGGATCAATCTCAGCTGGTGGCAACAA 336
Db 121 KTGAGGAAGGCACCTCCACAGCAAAACCTCGGATCAATCTCAGCTGGTGGCAACAA 180
QY 337 GTGGCACAACAGTATGCCACCCCAACCCCTTAAAAAGGAGAGAGAGAGAGAGAGAG 396
Db 181 GTGGCACAACAGTATGCCACCCCAACCCCTTAAAAAGGAGAGAGAGAGAGAGAGAG 240
QY 397 AAGCAGGACAAAGAGAAACCTTCAGAAACAGGAAATAGTCTAGTGTACCAAGAA 456
Db 241 AAGCAGGACAAAGAGAAACCTTCAGAAACAGGAAATAGTCTAGTGTACCAAGAA 300
QY 457 AATACCAACAAAGAAACCAAAACCAAGTCTGACATCTCTGAAAGATCTCTTAGTGAAGCA 516
Db 301 AATACCAACAAAGAAACCAAAACCAAGTCTGACATCTCTGAAAGATCTCTTAGTGAAGCA 359
QY 517 AACGATACAGTCTGCAAAATGCTACAAAGACACAGCAAGCAAGCAAGCAAGCAAGCA 576
Db 360 AACGATACAGTCTGCAAAATGCTACAAAGACACAGCAAGCAAGCAAGCAAGCAAGCA 419
QY 577 CCCCGGCTGAAAAACGT-GGACAGGAGCACTGACAGCAGTGG 619
Db 420 CCCCGGCTGAAAAACGTGGGACAGGAGCACTGACAGCAGTGG 463

RESULT 10
US-10-222-020-12
; Sequence 12, Application US/10222020
; Publication No. US20030175739A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT08C2
; CURRENT APPLICATION NUMBER: US/10/222,020
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/116,016
; PRIOR FILING DATE: 2003-04-05
; PRIOR APPLICATION NUMBER: 09/764,848
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17

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;; PRIOR APPLICATION NUMBER: 60/249,211
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,215
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,264
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,214
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,297
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/232,400
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/231,242
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,081
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,080
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,414
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,244
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,064
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/233,063
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,397
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,399
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,401
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,826
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08

Query Match 38.5%; Score 436; DB 16; Length 719;
Best Local Similarity 98.7%; Pred. No. 1.2e-118;
Matches 458; Conservative 2; Mismatches 2; Gaps 2;
QY 157 AAGAAGACCCGACAGGCGCAAAAGACAGGAAACCTGCGGACAGCAAGGGTTTGG 216
Db 1 AAGAAGACCCGACAGGCGCAAAAGACAGGAAACCTGCGGACAGCAAGGGTTTGG 60
QY 217 GATTGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCTTTAAATGCGAGCATCTGCCAT 276
Db 61 GATTGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCTTTAAATGCGAGCATCTGCCAT 120
QY 277 GTGAGGAAGGCACCTCCACCAAGAAAACCTCGGATCAATTCTCAGCTGGTGCCACAA 336
Db 121 KTGAGGAAGGCACCTCCACCAAGAAAACCTCGGATCAATTCTCAGCTGGTGCCACAA 180

QY 337 GTGGCACAACAGTATGCCACCCACCACCCCTAAAAAGCAGAGAAAGGAGAAAGTTGAA 396
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 GTGGCACAACAGTATGCCACCCACCACCCCTAAAAAGCAGAGAAAGGAGAAAGTTGAA 240
QY 397 AAGCAGGACAAAGAGAAACCTTGAGAAAGACAAGGAAATTAGTCTCTAGTGTTCACCAAGAA 456
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 AAGCAGGACAAAGAGAAACCTTGAGAAAGACAAGGAAATTAGTCTCTAGTGTTCACCAAGAA 300
QY 457 AATACCAACAAAGAAACCAAAACCAAGTCTGCACATTTCTGAAAGATCTCTCTAGTGAAGCA 516
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 AATACCAACAAAGAAACCAAAACCAAGTCTGCACATTTCTGAAA-ATCCTCTCTAGTGAAGCA 359
QY 517 AACAGCATACAGTCTGCAAAATGCTACAAAGACCAAGCAGCGAAACAAATFCACACCTCAAGG 576
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
360 AACAGCATACAGTCTGCAAAATGCTACAAAGACCAAGCAGCGAAACAAATFCACACCTCAAGG 419
QY 577 CCCCAGCTGAAAAACGT-GGACAGGAGCAGTGCACAGCAGTTGG 619
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
420 CCCCAGCTGAAAAACGTGGGACAGGAGCAGTGCACAGCGTTGG 463

RESULT 11
US-09-864-761-4575/c
; Sequence 4575, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

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; SEQ ID NO 4575
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012553.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
US-09-864-761-4575

Query Match      37.8%; Score 427.4; DB 9; Length 429;
Best Local Similarity 99.8%; Pred. No. 3.2e-116;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 586 AAAAAAGTGGACAGGACATCGACAGCAGTTGGCAGTAATCTGTGGGCAACGTCACCGTC 645
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QY 646 ATTATCAGACAGCTTTAAGGAAAGACTCGCTCTCATCGACATCTCTATCCACAGTGACC 705
DB 369 ATTATCAGACAGCTTTAAGGAAAGACTCGCTCTCATCGACATCTCTATCCACAGTGACC 310

QY 706 TCAGTGCAGGCTCAGAACAGCAGACAGAGCAGCTCGGGGTGAGAGACAGACAGCAAG 765
DB 309 TCAGTGCAGGCTCAGAACAGCAGACAGAGCAGCTCGGGGTGAGAGACAGACAGCAAG 250

QY 766 GGTCTCTCCCGTTCCTCCACGCCAAAGGCCGACATGTGACAGTCAATGATCAATCTTTG 825
DB 249 GGTCTCTCCCGTTCCTCCACGCCAAAGGCCGACATGTGACAGTCAATGATCAATCTTTG 190

QY 826 TGAATTCACATGGAATTTGTGAACACTATGATCAGGTATGAAATTCAAAACCTCCAC 885
DB 189 TGAATTCACATGGAATTTGTGAACACTATGAAATCAGGTATGAAATTCAAAACCTCCAC 130

QY 886 CTGCCCATCTGCTTCATCTCCCTGGAGAAATCTTGTGTGACATCGACCTCTTAGTGATGC 945
DB 129 CTGCCCATCTGCTTCATCTCCCTGGAGAAATCTTGTGTGACATCGACCTCTTAGTGATGC 70

QY 946 TGCCAGGATAATTTCTGTGTCATGGGCATCTGGCCACCAAGGAATTTGCAACCTGAC 1005
DB 69 TGCCAGGATAATTTCTGTGTCATGGGCATCTGGCCACCAAGGAATTTGCAACCTGAC 10

QY 1006 GATTACTCT 1014
DB 9 GATTACTCT 1

RESULT 12
US-10-505-680-571
; Sequence 571, Application US/10505680
; Publication No. US20050095592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.
; APPLICANT: Boyd, Jeff
; APPLICANT: Liu, Edison T.
; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TA
; FILE REFERENCE: 4239-64452
; CURRENT APPLICATION NUMBER: US/10/505,680
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/357,031
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 822
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 571
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(467)
; OTHER INFORMATION: "n" represents an unknown nucleotide
US-10-505-680-571

Query Match      29.8%; Score 337.4; DB 21; Length 467;
Best Local Similarity 93.4%; Pred. No. 2.1e-89;
Matches 424; Conservative 0; Mismatches 29; Indels 11; Gaps 6;

QY 75 CCACGAGGCTTTCTCTCCGAGCGCGCGCTTTTCGGCTTGGGGGGGGGGGTACAG 134
DB 5 CCCGAGCGGCTTCTCTCCGAGCGCGCGCTTTTCGGCTTGGGGGGGGGGGTACAG 64

QY 135 CCCATCCATGACCATGGGCGCAAGAGAGCGCCGACGAGCCCAAAAAGACGACGAAACC 194
DB 65 -CCATCCATGACCATGGGCGCAAGAGAGCGCCGACGAGCCCAAAAAGACGACGAAACC 123

QY 195 TGCCTCAGACCAAGGTTTTCGGGATTTAGCGTCTGCACCTTCAGAAAACAGTCTGAAAGC 254
DB 124 TGCCTCAGACCAAGGTTTTCGGGATTTAGCGTCTGCACCTTCAGAAAACAGTCTGAAAGC 183

QY 255 CTTTAAATGCAGCATCTCGGA-TGTGAGGAAAGGACCTCCACCAAGAAAACCTCGGATCA 313
DB 184 CTTTAAATGCAGCATCTCGGACTGTGAGGAAAGGACCTCCACCAAGAAAACCTCGGATCA 243

QY 314 ATTCTCAGCTGGTGACAAAGTGGGCAACAAGTGGGCAACAAGTGGGCAACAAGTGGGCAACA 373
DB 244 ATTCTCAGCTGGTGACAAAGTGGGCAACAAGTGGGCAACAAGTGGGCAACAAGTGGGCAACA 303

QY 374 AGGAGAAAGAGGAGAAAGTTG-AAAAGCAGGACAAA---GAGAACTCTGAGAAAGACAA 428
DB 304 AGGAGAAAGAGGAGAAAGTTGAAAGAAAGCAGGACAAAAGAGGAAAGTCTGAGAAAGACCAA 363

QY 429 GGAATATTAGTCC---TAGTGTGTACCAAGAAAATAACCAAGAAAACCAAAACCAAGTC 485
DB 364 GGAATATTAGTCTTAGTTGTGTACCAAGAAAATAACCAAGAAAACCAAAACCAAGTC 423

QY 486 TGACATTTGAAAGATCTCTCTAG-TGAAGCAAAACAGCATACAG 528
DB 424 TGACATTTTGAAGATCTCTCTAGTTGAAGCAAAACAGCATACAG 467

RESULT 13
US-10-505-680-570/c
; Sequence 570, Application US/10505680
; Publication No. US20050095592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.
; APPLICANT: Boyd, Jeff
; APPLICANT: Liu, Edison T.
; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC T
; FILE REFERENCE: 4239-64452
; CURRENT APPLICATION NUMBER: US/10/505,680
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/357,031
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 822
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 570
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(400)
; OTHER INFORMATION: "n" represents an unknown nucleotide
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US-10-505-680-570

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Query Match      28.0%; Score 316.6; DB 21; Length 400;
Best Local Similarity 93.5%; Pred. No. 3.1e-83;
Matches 375; Conservative 0; Mismatches 16; Indels 10; Gaps 4;

Qy 707 CCAGTGCAGGGTC-AGAACAGCAGAACACAGAGCAGCTCGGGGTCCAGAGAG-CCACAG 760
Db 400 CCAGTGCAGGGGTCAAGAACAGCAGAACACAGAGCAGCTCGGGGTCCAGAGAGCAGCGGAC 341

Qy 761 ACAAGGGTCTCTCCCGTTCCCT---CCAGCCAAAGGGGACATGTCAGCAGTCATATGATG 817
Db 340 AAAGGGCTTCCTCCCGTTCCCTTCNCAACCCCAAGGGGACATGTCAGCAGTCATATGATG 281

Qy 818 AATCTTTGTGAAATTGTCATGCAATGGAATTTGAAACATATGAATCAGGGTATGAATTTCAA 877
Db 280 AATCTTTGTGAAATTGTCATGCAATGGAATTTGAAACATATGAATCAGGGTATGAATTTCAA 221

Qy 878 ACCTCCACTGCCATGCTGCTTGCATCCCTGGGAATCTTCTGTGGACATCGACCTCTT 937
Db 220 ACCTCCACTGCCATGCTGCTTGCATCCCTGGGAATCTTCTGTGGACATCGACCTCTT 161

Qy 938 AGTGATGCTGCCAGGATAATTTCTGCTTGCATCGGCATCTGGCCACCAAGGAATTTTCGC 997
Db 160 AGTGATGCTGCCAGGATAATTTCTGCTT-NCATGGGCATCTGGCCACCAAGGAATTTTCGC 102

Qy 998 ACCCTGACGATTACTCTTGACACTTTTATGTAATTCATCTGTTTATATGATTTTCTTAAC 1057
Db 101 ACCCTGACGATTACTCTTGACACTTTTATGTAATTCATCTGTTTATATGATTTTCTTAAC 42

Qy 1058 AATCATTTATATTCGATGTCCTGCTGAATCTACTTTTTAT 1098
Db 41 AATCATTTATATTCGATGTCCTGCTGAATCTACTTTTTAT 1
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RESULT 14

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US-10-242-535A-10941
; Sequence 10941, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10941
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-10941
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Query Match      25.3%; Score 285.6; DB 17; Length 326;
Best Local Similarity 98.6%; Pred. No. 4.6e-74;
Matches 288; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 174 GCCAAAAAGACAAGCGAAACCTGCCGACAGAGAGGGTTTTGGGATTTGTAGCGTCTGCAC 233
Db 35 GGCACGAGGACACAGCGAAACCTGCCGACAGAGAGGGTTTTGGGATTTGTAGCGTCTGCAC 94

Qy 234 CTTCAGAAACAGTCTCTGAAAGCCTTTTAAATGTCAGCATCTCGCATGTGAGGAAAGGCACCTC 293
Db 95 CTTCAGAAACAGTCTCTGAAAGCCTTTTAAATGTCAGCATCTCGCATGTGAGGAAAGGCACCTC 154

Qy 294 CACCAGAAAACCTCGGATCAATTTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGC 353
Db 155 CACCAGAAAACCTCGGATCAATTTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGC 214

Qy 354 CACCCCAACCCCTTAAAGAGAGAGAGAGAGAGTTGAAAAGCAGGACAAAGAGAA 413
Db 215 CACCCCAACCCCTTAAAGAGAGAGAGAGAGAGTTGAAAAGCAGGACAAAGAGAA 274

Qy 414 ACCTGAGAAAGACAAGGAAATTTAGTCTCTAGTGTTCACAAAGAAAATACCAAC 465
Db 275 ACCTGAGAAAGACAAGGAAATTTAGTCTCTAGTGTTCACAAAGAAAATACCAAC 326
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RESULT 15

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US-10-085-783A-10941
; Sequence 10941, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10941
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-10941
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Best Local Similarity 98.6%; Pred. No. 4.6e-74;
Matches 288; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 174 GCCAAAAAGACAAGCGAAACCTGCCGACAGAGAGGGTTTTGGGATTTGTAGCGTCTGCAC 233
Db 35 GGCACGAGGACACAGCGAAACCTGCCGACAGAGAGGGTTTTGGGATTTGTAGCGTCTGCAC 94

Qy 234 CTTCAGAAACAGTCTCTGAAAGCCTTTTAAATGTCAGCATCTCGCATGTGAGGAAAGGCACCTC 293
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Qy	294	CACCGAAGAACTCGGATCAATTCTCAGCTGGCGCACACAAAGTGGCACACAGTATGC	353
Db	155	CACCGAAGAACTCGGATCAATTCTCAGCTGGCGCACACAAAGTGGCACACAGTATGC	214
Qy	354	CACCCACACACCCCTTAAAGGAGAGAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAA	413
Db	215	CACCCACACACCCCTTAAAGGAGAGAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAA	274
Qy	414	ACCTGAGAGAGACAAAGGAAATTAGTCTTAGTTACCAAGAAAATACCAAC	465
Db	275	ACCTGAGAGAGACAAAGGAAATTAGTCTTAGTTACCAAGAAAATACCAAC	326

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OM nucleic - nucleic search, using sw model

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Perfect score: 947
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Scoring table: IDENTITY_NUC
Gapop 10.0 Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_pr:*
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11: gb_sts:
12: gb_sy:*
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14: gb_vl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	944.2	99.7	947	6	AX092138	Sequence	
2	944.2	99.7	947	6	AX114151	Sequence	
3	944.2	99.7	947	6	AX138318	Sequence	
4	944.2	99.7	947	6	AX138324	Sequence	
5	883	93.2	1131	6	AX092139	Sequence	
6	883	93.2	1131	6	AX138319	Sequence	
7	883	93.2	1131	6	AX138332	Sequence	
8	881.4	93.1	1131	6	AX114152	Sequence	
9	871.2	92.0	2344	9	BC036459	Homo sapi	
10	870	91.9	943	6	CQ715417	Sequence	
11	870	91.9	1021	9	AY228125	Homo sapi	
12	870	91.9	1128	9	BC014959	Homo sapi	
13	870	91.9	3641	6	BD209971	Human tra	
14	868.4	91.7	1036	6	BCX821956	Sequence	
15	868.4	91.7	1036	9	AF179286	Homo sapi	
16	866.8	91.5	4700	9	AB029551	Homo sapi	
17	844	89.1	936	9	AF227959	Homo sapi	
18	730	77.1	4394	10	BC053016	Mus musc	
19	730	77.1	4472	10	BC080287	Mus musc	

20	726.8	76.7	201844	2	AC132261	Mus muscu
21	562.6	59.4	882	10	AF101779	Mus muscu
22	545.6	57.6	549	9	HUMV144E12	AF005840 Homo sapi
C 23	533.4	56.3	139207	2	AC069212	AC069212 Homo sapi
24	533.4	56.3	178219	9	AC104330	AC104330 Homo sapi
25	438.8	46.3	232891	2	AC117595	Mus muscu
C 26	433.2	45.7	188281	2	AC121030	AC121030 Rattus no
27	433.2	45.7	229752	2	AC127045	AC127045 Rattus no
C 28	428.6	45.3	429	6	CQ053717	Sequence
C 29	428.6	45.3	429	6	CQ068876	Sequence
C 30	428.6	45.3	429	6	CQ095936	Sequence
C 31	428.6	45.3	429	6	CQ134678	Sequence
C 32	428.6	45.3	429	6	CQ173179	Sequence
C 33	428.6	45.3	429	6	CQ202367	Sequence
C 34	428.6	45.3	429	6	CQ217944	Sequence
C 35	428.6	45.3	429	6	CQ256519	Sequence
C 36	428.6	45.3	429	6	CQ293610	Sequence
C 37	428.6	45.3	429	6	CQ330531	Sequence
C 38	428.6	45.3	429	6	CQ330531	Sequence
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C 39	232.4	24.5	253	6	CQ058707	Sequence
C 40	232.4	24.5	253	6	CQ078070	Sequence
C 41	232.4	24.5	253	6	CQ109071	Sequence
C 42	232.4	24.5	253	6	CQ147699	Sequence
C 43	232.4	24.5	253	6	CQ183070	Sequence
C 44	232.4	24.5	253	6	CQ207485	Sequence
C 45	232.4	24.5	253	6	CQ230949	Sequence

ALIGNMENTS

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RESULT 1
AX092138
LOCUS      AX092138            linear       PAT 21-MAR-2001
DEFINITION Sequence 8 from Patent WO0116165.
ACCESSION  AX092138
VERSION    AX092138.1 GI:13444365
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  1
AUTHORS   Noteborn,M.H. and danen-van Oorschot,A.A.
TITLE     Apoptin-associating protein
JOURNAL   Patent: WO 0116165-A 8 08-MAR-2001;
          Leadd B.V. (NL)

FEATURES   Location/Qualifiers
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                                /db_xref="taxon:9606"
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                                /note="'AAP-1-a nucleic acid wherein N can be A, C, G or
                                T,'"

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Query Match          99.7%; Score 944.2; DB 6; Length 947;
Best Local Similarity 100.0%; Pred. NO. 1.4e-233;
Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 ACCANCCCAAAAAGAGATCTGGAAATTCGGATCCTCGAGGCCACCAAGGCGCGAAACAG 60
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Qy  61 TGCTGAAGCCTTTAAATGCAGCATCTCGCATGTGAGGAAAGGCCACTTCCACCAGAAAAACC 120
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    |||

Qy  121 TCAGATCAATTCTCAGCTGGTGGGNCNCAAGAATGGGCAACAAGTAGTGCCACCCACCACC 180
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[illegible]

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LOCUS AXI38318 947 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 8 from Patent EP1083224.
ACCESSION AXI38318
VERSION AXI38318.1 GI:14274284
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Noteborn,M.H. and danen-van Oorschot,A.A.
TITILE Apoptin-associating protein
JOURNAL Patent: EP 1083224-A 8 14-MAR-2001;
Leadd B.V. (NL)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1..947
/notes="AAP-1-a nucleic acid wherein N can be A, C, G or T."
ORIGIN
Query Match 99.7%; Score 944.2; DB 6; Length 947;
Best Local Similarity 100.0%; Pred. No. 1.4e-233;
Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACCNACCCAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAGCCGGAACAG 60
Db 1 ACCNACCCAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAGCCGGAACAG 60
Qy 61 TGCTGAAGCCTTTAAATGCGATCTCGATCTGAGGAAAGGACCTCCACCGAAAC 120
Db 61 TGCTGAAGCCTTTAAATGCGATCTCGATCTGAGGAAAGGACCTCCACCGAAAC 120
Qy 121 TCGGATCAATTTCTCAGCTGTGGCNCACAAAGTGGGCAACAGATGCGACCCAC 180
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RESULT 4
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LOCUS AXI38324 947 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 4 from Patent EP1081226.
ACCESSION AXI38324
VERSION AXI38324.1 GI:14274287
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Noteborn,M.H. and danen-van Oorschot,A.A.
TITILE Apoptin-associating protein
JOURNAL Patent: EP 1081226-A 4 07-MAR-2001;
Leadd B.V. (NL)
FEATURES
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Qy 181 CCCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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Qy	901	ATCTACTTTTATAAAAAAGCCTTGTGGCTTCGAGAGATCTATGA	947		
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LOCUS	Sequence 9 from Patent WO0116165.				
DEFINITION	AX092139				
ACCESSION	AX092139				
VERSION	AX092139.1	GI:13444366			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Noteborn,M.H. and danen-van Oorschot,A.A.				
TITLE	Apoptin-associating protein				
JOURNAL	Patent: WO 0116165-A 9 08-MAR-2001;				
LEADD	Leadd B.V. (NL)				
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ORIGIN					
Query Match	93.2%;	Score 883;	DB 6;	Length 1131;	

[illegible]

AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haiech, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2344)	
AUTHORS	Strausberg, R.	
TITLE	Direct Submission	
JOURNAL	Submitted (09-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk Email: cgap@remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org Contact: amadanasystemsbio.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting	
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAP Plate: 46 Row: e Column: 4.	
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ACCESSION	C0715417												
VERSION	C0715417.1	GI:42276274											
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SOURCE	Homo sapiens (human)												
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.												
	1												
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.												
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	humanexons or transcripts, for detecting expression and other uses												
TITLE	thereof												
	Patent: WO 02068579-A 1351 06-SEP-2002;												
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Qy	264	CCAGAAAATATCCACAGAAACCAACCAAGTCTGACATCTCGAAGATCCTCCTTA	323										
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Qy	384	CCTCAAGGCCCGCTGAAAACCGTGACAGGAGCACTGCACAGCAGTTGGCAGTAAC TG	443										
Db	402	CCTCAAGGCCCGCTGAAAACCGTGACAGGAGCACTGCACAGCAGTTGGCAGTAAC TG	461										
Qy	444	TGGCAACGTCACGTCATTTATCACAGACTTTAAGGAAAGACTCGCTCTCTCATGCAT	503										
Db	462	TGGCAACGTCACGTCATTTATCACAGACTTTAAGGAAAGACTCGCTCTCTCATGCAT	521										
Qy	504	CCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAAACCCAGCAGCTCGGGGT	563										
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DEFINITION	Homo sapiens apoptin-associating protein 1 (AAP1) mRNA, complete cds.		
ACCESSION	AY228125		
VERSION	AY228125.1	GI:29423710	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1021)		
AUTHORS	Danen-van Oorschot, A.A.M., Voskamp, P., Seelen, M.C., van Miltenburg, M.H., Bolk, M.W., Tait, S.W., Boesen-de Cock, J.G., Rohn, J.L., Borst, J. and Noteborn, M.H.		
TITLE	Human death effector domain-associated factor interacts with the viral apoptosis agonist Apoptin and exerts tumor-preferential cell killing		
JOURNAL	Cell Death Differ. 11 (5), 564-573 (2004)		
PUBMED	14765135		
REFERENCE	2 (bases 1 to 1021)		
AUTHORS	Danen-van Oorschot, A.A.M., Boesen-de Cock, J.G.R., Borst, J. and Noteborn, M.H.M.		
TITLE	AAP-1, a binding partner of Apoptin, induces cell death in human tumor cells but not in normal diploid cells		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1021)		
AUTHORS	Danen-van Oorschot, A.A.M., Boesen-de Cock, J.G.R., Borst, J. and Noteborn, M.H.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-JAN-2003) Leadd BV, Wassenaarseweg 72, Leiden 2333		
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Qy 84 TCTGCGATGTGAGAAAGGACCTCCACCAAGAAACCTCGATCAATTTCTAGCTGGTG 143
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Qy 864 TTTCTTAACATCAATTTATATGATGATGCTCTGATCTGATCTACTTTTATAAAAA 920
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RESULT 12
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DEFINITION Homo sapiens RING1 and YY1 binding protein, mRNA (cDNA clone
MGC:23015 IMAGE:4902201), complete cds.
ACCESSION BC014959
VERSION BC014959.1 GI:15928992
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1128)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vialalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pachter, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1128)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smalius, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at: <http://image.llnl.gov>

Series: IRAL Plate: 34 Row: 0 Column: 8

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24432049.

FEATURES

Location/Qualifiers

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gene

CDS

REFERENCE	2 (bases 1 to 1036)	
AUTHORS	Zheng,L.X., Yoo,T. and Lenardo,M.J.	
TITLE	A novel protein associated with Caspase-10 DED domain	
JOURNAL	Unpublished	
REFERENCE	3 (bases 1 to 1036)	
AUTHORS	Zheng,L.X., Yoo,T. and Lenardo,M.J.	
TITLE	Direct Submission	
JOURNAL	Submitted (20-AUG-1999) NIAID/LI, NIH, 9000 Rockville Pike, Bethesda, MD 20892, USA	
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ORIGIN		
Query Match	91.7%; Score 868.4; DB 9; Length 1036;	
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Matches	878; Conservative 1; Mismatches 18; Indels 0; Gaps 0;	
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 03:14:16 ; Search time 580.596 Seconds
(without alignments)
9655.591 Million cell updates/sec

Title: US-09-655-109a-4

Perfect score: 947

Sequence: 1 accanaccacaaaaaagaga.....tggcctcgagagatctatga 947

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: Geneseqn2001as:*
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- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	944.2	99.7	947	4	Aaf55404 Nucleotid
3	944.2	99.7	947	5	Aaf57184 Apoptin-a
4	883	93.2	1131	4	Aaf55596 Nucleotid
5	883	93.2	1131	4	Aaf55405 Nucleotid
6	883	93.2	1131	5	Aaf57185 Apoptin-a
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8	870	91.9	3641	3	Aaz52452 HTRM clon
9	868.4	91.7	1036	10	Adk66994 Gene #84
10	868.4	91.7	1036	10	Adk61399 Ovarian c
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12	859	90.7	2156	4	Aas34877 cDNA enco
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15	428.6	45.3	429	4	Aai14743 Probe #46
16	428.6	45.3	429	4	Aas56475 Human foe
17	428.6	45.3	429	4	Aai36109 Probe #47
18	428.6	45.3	429	4	Aba45949 Human bre
19	428.6	45.3	429	4	Aba26109 Probe #45
20	428.6	45.3	429	4	Aak30143 Human bon

C 21	428.6	45.3	429	4	AAK04634	Aak04634 Human bra
C 22	428.6	45.3	429	4	ABS29793	Abs29793 Human liv
C 23	428.6	45.3	429	5	AAI04546	Aai04546 Probe #45
C 24	428.6	45.3	429	6	ABS04724	Abso4724 Human gen
25	386	40.8	1501	5	AAS87102	Aas87102 DNA enco
26	357.4	37.7	719	4	AAS35003	Aas35003 cDNA enco
27	357.4	37.7	719	4	ABK43152	Abk43152 cDNA enco
28	357.4	37.7	719	10	ADC46161	Adc46161 Human neo
29	317.8	33.6	400	10	ADK61400	Adk61400 Ovarian c
30	255.8	27.0	515	5	AAS80294	Aas80294 DNA enco
31	232.4	24.5	253	4	AAI23937	Aai23937 Probe #13
32	232.4	24.5	253	4	ABA69056	Aba69056 Human foe
33	232.4	24.5	253	4	AAI49244	Aai49244 Probe #17
34	232.4	24.5	253	4	ABA51067	Aba51067 Human bre
35	232.4	24.5	253	4	ABA36000	Aba36000 Probe #14
36	232.4	24.5	253	4	AAK43164	Aak43164 Human bon
37	232.4	24.5	253	4	AAK17369	Aak17369 Human bra
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40	232.4	24.5	253	6	ABS17240	Abs17240 Human gen
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ALIGNMENTS

RESULT 1

AAF55595
ID AAF55595 standard; cDNA; 947 BP.

AC AAF55595;

XX 29-MAY-2001 (first entry)

XX Nucleotide sequence of apoptin-associating protein 1 cDNA clone a.

XX Apoptin-associating protein; AAP; apoptosis; cell proliferation;
cell death; autoimmune disease; cancer; ss.

XX Homo sapiens.

XX W0200116165-A2.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-NL000612.

XX 02-SEP-1999; 99EP-00202858.

XX 21-OCT-1999; 99EP-00203465.

XX (LEAD-) LEADD BV.

XX Noteborn MHM, Danen-Van Oorschot AAAM;

XX WPI; 2001-235090/24.

XX New nucleic acids encoding apoptin-associating proteins useful for
inducing apoptosis, particularly p53 independent apoptosis, or for
treating cancers or autoimmune diseases.

XX Claim 6; Fig 1; 50pp; English.

XX The present sequence encodes a human apoptin-associating protein 1
(AAP1). The protein is capable of providing apoptosis. AAP polypeptides
and polynucleotides are useful for inducing apoptosis, particularly when
apoptosis is p53-independent. They may be used to produce pharmaceutical
compositions which are used for treating a disease where enhanced cell
proliferation or decreased cell death is observed, particularly in cancer
or in autoimmune diseases, for diagnosing a disease related with

CC	aberrancies in the apoptotic process, and for detecting the presence of									
CC	cancer cells or cells that are prone to cancer									
XX										
SQ	Sequence	947 BP;	309 A;	238 C;	198 G;	198 T;	0 U;	4 Other;		
	Query Match	99.7%; Score 944.2; DB 4; Length 947;								
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Qy	901	ATCTACTTTTTTATAAAAAAGCCTTGTGGCCTCGAGAGATCTATGA	947							
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RESULT 2	
AAF55404	
ID	AAF55404 standard; DNA; 947 BP.
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AC	AAF55404;
DT	29-MAY-2001 (first entry)
XX	
DE	Nucleotide sequence of an apoptin-associating protein.
XX	
KW	Apoptin-associating proteinaceous substance; cell proliferation;
KW	apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer;
XX	autoimmune disease; 88.
OS	Homo sapiens.
XX	
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CDS	
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FT	402..440
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FT	519..884
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XX	
EP1081226-A1.	
PN	
XX	
PD	07-MAR-2001.
XX	
PF	02-SEP-1999; 99EP-00202858.
XX	
PR	02-SEP-1999; 99EP-00202858.
XX	
PA	(LEAD-) LEADD BV.
XX	
DR	WPI; 2001-219813/23.
DR	P-PSDB; AAB67552, AAB67553, AAB67554, AAB67555, AAB67556, AAB67557,
DR	AAB67558.
XX	
PT	Novel isolated or recombinant apoptin-associating proteinaceous
PT	substance, apoptin-associating protein 1, useful for inducing apoptosis
PT	for treating cancer or autoimmune diseases caused by aberrant apoptosis.
XX	
PS	Claim 4; Fig 1; 29pp; English.
XX	
CC	The present sequence encodes an apoptin-associating proteinaceous
CC	substance (apoptin-associating protein 1 (AAP-1)), which is capable of
CC	inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for
CC	inducing a p53-independent apoptosis. They are used for treating a
CC	disease where enhanced proliferation or decreased cell death is observed
CC	e.g. cancer or autoimmune disease. They are also used for diagnosis of
CC	diseases related with aberrations in the apoptotic process such as cancer
CC	and autoimmune diseases
XX	
SQ	Sequence 947 BP; 309 A; 238 C; 198 G; 198 T; 0 U; 4 Other;

Query Match		99.7%; Score 944.2; DB 4; Length 947;
Best Local Similarity		100.0%; Pred. No. 7.9e-250;
Matches 947; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	ACCANACCCAAAAAGAGATCTGGAAATTCGGATTCCTCGAGGCCACGAAGGCCGAAACAG 60
Db	1	ACCANACCCAAAAAGAGATCTGGAAATTCGGATTCCTCGAGGCCACGAAGGCCGAAACAG 60
Qy	61	TGCTGAAGCCTTTAAATGCGAGCATCTCGATGTGAGGAAGGACCTCCACCGAAGAAC 120
Db	61	TGCTGAAGCCTTTAAATGCGAGCATCTCGATGTGAGGAAGGACCTCCACCGAAGAAC 120
Qy	121	TCGGATCAATTCCTCAGCTGGTGGCNCACAAAGTGGCAACAAGTGGCACACAGTATGCCACCCACC 180
Db	121	TCGGATCAATTCCTCAGCTGGTGGCNCACAAAGTGGCAACAAGTGGCACACAGTATGCCACCCACC 180
Qy	181	CCCTAAAGAGGAGAGAGAGAAAGTTGAAAAGCGAGGACAAAGAGAACTCTGAGAAGA 240
Db	181	CCCTAAAGAGGAGAGAGAGAAAGTTGAAAAGCGAGGACAAAGAGAACTCTGAGAAGA 240
Qy	241	CAAGGAATTTAGTCTCTAGTGTTCACCAAGAAATATCCCAAGAAACCAACCAAGTC 300
Db	241	CAAGGAATTTAGTCTCTAGTGTTCACCAAGAAATATCCCAAGAAACCAACCAAGTC 300
Query Match		99.7%; Score 944.2; DB 5; Length 947;
Best Local Similarity		100.0%; Pred. No. 7.9e-250;
Matches 947; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	ACCANACCCAAAAAGAGATCTGGAAATTCGGATTCCTCGAGGCCACGAAGGCCGAAACAG 60
Db	1	ACCANACCCAAAAAGAGATCTGGAAATTCGGATTCCTCGAGGCCACGAAGGCCGAAACAG 60
Qy	61	TGCTGAAGCCTTTAAATGCGAGCATCTCGATGTGAGGAAGGACCTCCACCGAAGAAC 120
Db	61	TGCTGAAGCCTTTAAATGCGAGCATCTCGATGTGAGGAAGGACCTCCACCGAAGAAC 120
Qy	121	TCGGATCAATTCCTCAGCTGGTGGCNCACAAAGTGGCAACAAGTGGCACACAGTATGCCACCCACC 180
Db	121	TCGGATCAATTCCTCAGCTGGTGGCNCACAAAGTGGCAACAAGTGGCACACAGTATGCCACCCACC 180
Qy	181	CCCTAAAGAGGAGAGAGAGAAAGTTGAAAAGCGAGGACAAAGAGAACTCTGAGAAGA 240
Db	181	CCCTAAAGAGGAGAGAGAGAAAGTTGAAAAGCGAGGACAAAGAGAACTCTGAGAAGA 240
Qy	241	CAAGGAATTTAGTCTCTAGTGTTCACCAAGAAATATCCCAAGAAACCAACCAAGTC 300
Db	241	CAAGGAATTTAGTCTCTAGTGTTCACCAAGAAATATCCCAAGAAACCAACCAAGTC 300
Qy	301	TGACATTCGAAAGATCTCTAGTGAAGCAACAGCATACAGTCTGCAATGCTACAAC 360
Db	301	TGACATTCGAAAGATCTCTAGTGAAGCAACAGCATACAGTCTGCAATGCTACAAC 360
Qy	361	AAAGACCGGCAAAACAAATCACACCTCAAGCCCGGCTGAAAACCTGGACAGGAGCAC 420
Db	361	AAAGACCGGCAAAACAAATCACACCTCAAGCCCGGCTGAAAACCTGGACAGGAGCAC 420
Qy	421	TGCACAGCTGGCAGTAACTGTGGGCAAGTCAACGTCATTTATCACAGACTTTAAGGA 480
Db	421	TGCACAGCTGGCAGTAACTGTGGGCAAGTCAACGTCATTTATCACAGACTTTAAGGA 480
Qy	481	AAAGACTCGCTCTCATCGACATCCTCATCACAGTGACCTTCCAGTCCAGGGTCAGAAACA 540
Db	481	AAAGACTCGCTCTCATCGACATCCTCATCACAGTGACCTTCCAGTCCAGGGTCAGAAACA 540
Qy	541	GCAGAACGACAGSACGCTCGGGTCAGAGACACAGCAAGGGCTCTCCCGTTCTCTCCAC 600
Db	541	GCAGAACGACAGSACGCTCGGGTCAGAGACACAGCAAGGGCTCTCCCGTTCTCTCCAC 600
Qy	601	GCCAAAGGGGACATGTCAGCAGTCAATGATGATCTTTCTGAAATTCGACATGGAAATG 660
Db	601	GCCAAAGGGGACATGTCAGCAGTCAATGATGATCTTTCTGAAATTCGACATGGAAATG 660
Qy	661	TGAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGTGCATC 720
Db	661	TGAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGTGCATC 720
Qy	721	CCTGGAGAATCTCTGTGGACATCGACCTCTTAGTGATGTCGCCAGGATAATTTCTGCTT 780
Db	721	CCTGGAGAATCTCTGTGGACATCGACCTCTTAGTGATGTCGCCAGGATAATTTCTGCTT 780
Qy	781	GCCATGGGCATCTGGCCACCAAGGAATTCGCCACCTGACGATTAATCTTGGACACTTTTA 840
Db	781	GCCATGGGCATCTGGCCACCAAGGAATTCGCCACCTGACGATTAATCTTGGACACTTTTA 840
Qy	841	TGTAATTCATTTTATATGATTTCTCTAACAATCATTTATATATGATGTCCTCTGA 900
Db	841	TGTAATTCATTTTATATGATTTCTCTAACAATCATTTATATATGATGTCCTCTGA 900
Qy	901	ATCTACTTTTTTAAAAAGCCTTGTGGCCTCGAGAGATCTATGA 947
Db	901	ATCTACTTTTTTAAAAAGCCTTGTGGCCTCGAGAGATCTATGA 947
RESULT 3		
AAF57184		
ID		AAF57184 standard; cDNA; 947 BP.
XX		

AC	AAF57184;
XX	29-MAY-2001 (first entry)
XX	Apoptin-associating protein (AAP)-1-a nucleotide sequence.
DE	Apoptin-associating protein; AAP; apoptosis; p53; cell proliferation;
XX	cell death; cancer; autoimmune disease; cytostatic; immunosuppressive;
KW	gene therapy; AAP-1-a; ss.
XX	Homo sapiens.
OS	EP1083224-A2.
PN	14-MAR-2001.
XX	01-SEP-2000; 2000EP-00203042.
PF	02-SEP-1999; 99EP-00202858.
XX	21-OCT-1999; 99EP-00203465.
PR	(LEAD-) LEADD BV.
XX	Noteborn MM, Danen-Van Oorschot AAAM;
PI	WPI; 2001-228257/24.
XX	New nucleic acids encoding apoptin-associating proteins capable of
XX	inducing p52 independent apoptosis, useful for treating a disease
PT	associated with enhanced cell proliferation or decreased cell death, e.g.
PT	cancer or autoimmune disease.
XX	Claim 6; Fig 1; 26pp; English.
PS	The invention provides isolated or recombinant nucleic acid (I), its
XX	functional encoding an apoptin-associating proteinaceous (AAP) substance
CC	capable of apoptosis. (I), the vector comprising (I), the host cell
CC	comprising the vector and the proteinaceous substance encoded by (I) are
CC	useful for inducing apoptosis, particularly p53-independent apoptosis,
CC	and for treating a disease where enhanced cell proliferation or decreased
CC	cell death is observed, such as cancer or an autoimmune disease. A
CC	composition comprising the nucleic acid or the AAP may further be used
CC	for diagnosing a disease related with aberrancies in the apoptotic
CC	process, and for detecting the presence of cancer cells or cells that are
CC	prone to cancer. The present sequence represents the nucleotide sequence
CC	of the AAP-1-a cDNA clone
XX	Sequence 947 BP; 309 A; 238 C; 198 G; 198 T; 0 U; 4 Other;
Qy	Query Match 99.7%; Score 944.2; DB 5; Length 947;
Db	Best Local Similarity 100.0%; Pred. No. 7.9e-250;
Db	Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ACCNACCCAAAAAGAGATCTGGAAATTCGGATTCCTCGAGGCCACGAAGGCCGAAACAG 60
Db	1 ACCNACCCAAAAAGAGATCTGGAAATTCGGATTCCTCGAGGCCACGAAGGCCGAAACAG 60
Qy	61 TGCTGAAGCCTTTAAATGCGAGCATCTCGATGTGAGGAAGGACCTCCACCGAAGAAC 120
Db	61 TGCTGAAGCCTTTAAATGCGAGCATCTCGATGTGAGGAAGGACCTCCACCGAAGAAC 120
Qy	121 TCGGATCAATTCCTCAGCTGGTGGCNCACAAAGTGGCAACAAGTGGCACACAGTATGCCACCCACC 180
Db	121 TCGGATCAATTCCTCAGCTGGTGGCNCACAAAGTGGCAACAAGTGGCACACAGTATGCCACCCACC 180
Qy	181 CCCTAAAGAGGAGAGAGAAAGTTGAAAAGCGAGGACAAAGAGAACTCTGAGAAGA 240
Db	181 CCCTAAAGAGGAGAGAGAAAGTTGAAAAGCGAGGACAAAGAGAACTCTGAGAAGA 240
Qy	241 CAAGGAATTTAGTCTCTAGTGTTCACCAAGAAATATCCCAAGAAACCAACCAAGTC 300
Db	241 CAAGGAATTTAGTCTCTAGTGTTCACCAAGAAATATCCCAAGAAACCAACCAAGTC 300

Qy 301 TGACATCTGAAGATCCTCTAGTGAAGCAAAACAGACATACAGTCTGCAAAATGCTCAAC 360
Db |||||||
Qy 301 TGACATCTGAAGATCCTCTAGTGAAGCAAAACAGACATACAGTCTGCAAAATGCTCAAC 360
Db |||||||
Qy 361 AAAGACACGAGGAACAAATACACACTCAAGGCCCGGCTGAAAAAACGTGACAGGAGCAC 420
Db |||||||
Qy 361 AAAGACACGAGGAACAAATACACACTCAAGGCCCGGCTGAAAAAACGTGACAGGAGCAC 420
Db |||||||
Qy 421 TGCACAGCTGGGCACTAATGTGGGCAACGTCACCGTCATTATACACAGACTTTAAGGA 480
Db |||||||
Qy 421 TGCACAGCTGGGCACTAATGTGGGCAACGTCACCGTCATTATACACAGACTTTAAGGA 480
Db |||||||
Qy 481 AAAGACTCGTCTCTATCGACATCTCATCCACAGTGAACCTCCAGTGCAGGGTCAGAAC 540
Db |||||||
Qy 481 AAAGACTCGTCTCTATCGACATCTCATCCACAGTGAACCTCCAGTGCAGGGTCAGAAC 540
Db |||||||
Qy 541 GCAGAACACAGACAGCTCGGGGTGACAGAGACACAGCAAGGGCTCTCCCGTTCCTCCAC 600
Db |||||||
Qy 541 GCAGAACACAGACAGCTCGGGGTGACAGAGACACAGCAAGGGCTCTCCCGTTCCTCCAC 600
Db |||||||
Qy 601 GCCAAGGGGACATGTACAGCTCAATGATGAATCTTTCTGAAATGGACATGGAATTG 660
Db |||||||
Qy 601 GCCAAGGGGACATGTACAGCTCAATGATGAATCTTTCTGAAATGGACATGGAATTG 660
Db |||||||
Qy 661 TGAAGACTATGAATCAGGGTATGAATTCAAAACCTCCACCTGCCATGCTGCTTGCAATC 720
Db |||||||
Qy 661 TGAAGACTATGAATCAGGGTATGAATTCAAAACCTCCACCTGCCATGCTGCTTGCAATC 720
Db |||||||
Qy 721 CCTGGAGAACTCTTGTGGACATCGACCTCTTATGATGCTGCCAGGATAATTTCTGCTT 780
Db |||||||
Qy 721 CCTGGAGAACTCTTGTGGACATCGACCTCTTATGATGCTGCCAGGATAATTTCTGCTT 780
Db |||||||
Qy 781 GCATGGGGATCTGGCCACCAAGGAATTTGCAACCTTGACAGATTAATCTTTGACACTTTTA 840
Db |||||||
Qy 781 GCATGGGGATCTGGCCACCAAGGAATTTGCAACCTTGACAGATTAATCTTTGACACTTTTA 840
Db |||||||
Qy 841 TGTATTCATTTTATATATGATTTTCTTAACATCAATTTATATGATGCTGCTCTGA 900
Db |||||||
Qy 841 TGTATTCATTTTATATATGATTTTCTTAACATCAATTTATATGATGCTGCTCTGA 900
Db |||||||
Qy 901 ATCTACTTTTTATAAAAAGCCCTTGTGGCCCTCGAGAGATCTATGA 947
Db |||||||
Qy 901 ATCTACTTTTTATAAAAAGCCCTTGTGGCCCTCGAGAGATCTATGA 947
Db |||||||

RESULT 4
AAF55596
ID AAF55596 standard; cDNA; 1131 BP.
XX
AC AAF55596;
XX
AC AAF55596;
XX
DT 29-MAY-2001 (first entry)
XX
DE Nucleotide sequence of apoptin-associating protein 1 cDNA clone b.
XX
KW Apoptin-associating protein; AAP; apoptosis; cell proliferation;
KW cell death; autoimmune disease; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200116165-A2.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-NL000612.
XX
PR 02-SEP-1999; 99EP-00202858.
PR 21-OCT-1999; 99EP-00203465.
XX
PA (LEAD-) LEADD BV.
XX
PI Noteborn MHM, Danen-Van Oorschot AAAM;
XX

DR WPI; 2001-235090/24.
XX New nucleic acids encoding apoptin-associating proteins useful for
PT inducing apoptosis, particularly p53 independent apoptosis, or for
PT treating cancers or autoimmune diseases.
XX
PS Claim 6; Fig 2; 50pp; English.
XX
CC The present sequence encodes a human apoptin-associating protein 1
CC (AAP1). The protein is capable of providing apoptosis. AAP polypeptides
CC and polynucleotides are useful for inducing apoptosis, particularly when
CC apoptosis is p53-independent. They may be used to produce pharmaceutical
CC compositions which are used for treating a disease where enhanced cell
CC proliferation or decreased cell death is observed, particularly in cancer
CC or in autoimmune diseases, for diagnosing a disease related with
CC aberrancies in the apoptotic process, and for detecting the presence of
CC cancer cells or cells that are prone to cancer
XX
SQ Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
Query Match 93.2%; Score 883; DB 4; Length 1131;
Best Local Similarity 97.7%; Pred. No. 6.7e-233;
Matches 903; Conservative 2; Mismatches 18; Indels 1; Gaps 1;
Qy 24 GGAATTCGGATCTCGAGGCCACGAAGGCCGAAACAGTCTGAAGCCTTTAAATGCAGCA 83
Db |||||||
Qy 209 GGTITTTGGATTTAGCGTCTGCACCTTCAGAAACAGTCTGAAGCCTTTAAATGCAGCA 268
Db |||||||
Qy 84 TCTGCGATGTGAGGAAAGGCACCTCCACAGAAAAACCTCGGATCAATTTCTAGCTGGTG 143
Db |||||||
Qy 269 TCTGCGATGTGAGGAAAGGCACCTCCACAGAAAAACCTCGGATCAATTTCTAGCTGGTG 328
Db |||||||
Qy 144 CACAAACAGTGGCAACAGATATGCCACCCACACCCCTAAAAAGGAGAGAAAGAGA 203
Db |||||||
Qy 329 CACAAACAGTGGCAACAGATATGCCACCCACACCCCTAAAAAGGAGAGAAAGAGA 388
Db |||||||
Qy 204 AAGTTCAAAAGCAGGACAAAGAAACCTGAGAAAGCAAGGAAATTAGTCTAGTGTGA 263
Db |||||||
Qy 389 AAGTTGAAAAGCAGGACAAAGAAACCTGAGAAAGCAAGGAAATTAGTCTAGTGTGA 448
Db |||||||
Qy 264 CCAAGAAAAATACCAAACAGAAAAACCAAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 323
Db |||||||
Qy 449 CCAAGAAAAATACCAAACAGAAAAACCAAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 508
Db |||||||
Qy 324 GTGAACCAACAGACATACAGTCTGCAATGCTACAAAGACCAAGCCAGGAAACAAATCACA 383
Db |||||||
Qy 509 GTGAACCAACAGACATACAGTCTGCAATGCTACAAAGACCAAGCCAGGAAACAAATCACA 568
Db |||||||
Qy 384 CTTCAAGGCCCGGCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTGTGGCAGTAACCTG 443
Db |||||||
Qy 569 CTTCAAGGCCCGGCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTGTGGCAGTAACCTG 628
Db |||||||
Qy 444 TGGGCAACGTCAACCGTCATTATACAGACTTTTAAAGGAAAAGCTCGCTCTCTCATGACAT 503
Db |||||||
Qy 629 TGGGCAACGTCAACCGTCATTATACAGACTTTTAAAGGAAAAGCTCGCTCTCTCATGACAT 688
Db |||||||
Qy 504 CTTCAATCCACAGTGAACCTCCAGTGGAGGCTGAGAACAGCAGACCAAGCCAGCAGCTCGGGGT 563
Db |||||||
Qy 689 CTTCAATCCACAGTGAACCTCCAGTGGAGGCTGAGAACAGCAGACCAAGCCAGCAGCTCGGGGT 748
Db |||||||
Qy 564 CAGAGAGCACAGCAAGGGCTCTCCCGGTTCTCTCCACGGCCAAAGGCGGACATGTCAGCAG 623
Db |||||||
Qy 749 CAGAGAGCACAGCAAGGGCTCTCCCGGTTCTCTCCACGGCCAAAGGCGGACATGTCAGCAG 808
Db |||||||
Qy 624 TCAATGATGAATCTTTCTGAAATTTGCAATGGAATTTGGAATACTATGAATCAGGGTATG 683
Db |||||||
Qy 809 TCAATGATGAATCTTTCTGAAATTTGCAATGGAATTTGGAATACTATGAATCAGGGTATG 868
Db |||||||
Qy 684 AATTTCAAACCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 743
Db |||||||
Qy 869 AATTTCAAACCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 928
Db |||||||
Qy 744 CGACCTCTTAGTGAATGCTGCCAGGATAATTTTCTGCTTGCCATGGGATCTGGCCACCAAG 803
Db |||||||

Db 929 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTCCATGGGCATCTGGCCACCAAG 988
Qy 804 GAATTTCCGACCCCTGACGATTAATCTTGACACTTTTATGTAATCCATTGTTTATATGAT 863
Db 989 GAATTTCCGACCCCTGACGATTAATCTTGACACTTTTATGTAATCCATTGTTTATATGAT 1048
Qy 864 TTTCTTAAACATCAATTTATATATGATGCTCTGGAATCTACTTTTATATAAAAAAGCC 923
Db 1049 TTTCTTAAACATCAATTTATATATGATGCTCTGGAATCTACTTTTAT-AAAAAGGCC 1107
Qy 924 TTYGTGGCCTCGAGATCTATGA 947
Db 1108 TTCTGGCCTCGAGATCTATGA 1131

RESULT 5
AAF55405
ID AAF55405 standard; DNA; 1131 BP.
XX AAF55405;
AC AAF55405;
DT 29-MAY-2001 (first entry)
XX Nucleotide sequence of an apoptin-associating protein.
XX Apoptin-associating proteinaceous substance; cell proliferation;
KW apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer;
KW autoimmune disease; ss.
XX Homo sapiens.

XX Key Location/Qualifiers
FH 1..828
CDS /*tag= a
FT /note= "encodes AAB67559"
FT 829..939
FT /*tag= b
FT /note= "encodes AAB67560"
FT 943..1017
FT /*tag= c
FT /note= "encodes AAB67561"
FT 1018..1047
FT /*tag= d
FT /note= "encodes AAB67562"
FT 1057..1131
FT /*tag= e
FT /note= "encodes AAB67563"
XX
XX EP1081226-A1.
XX
XX 07-MAR-2001.
XX
XX 02-SEP-1999; 99EP-00202858.
XX
XX 02-SEP-1999; 99EP-00202858.
XX
XX (LEAD-) LEADD BV.
XX
XX WPI; 2001-219813/23.
XX P-PSDB; AAB67559, AAB67560, AAB67561, AAB67562, AAB67563.
XX Novel isolated or recombinant apoptin-associating proteinaceous
PT substance, apoptin-associating protein 1, useful for inducing apoptosis
PT for treating cancer or autoimmune diseases caused by aberrant apoptosis.
XX
XX Claim 4; Fig 2; 29pp; English.
XX
XX The present sequence encodes an apoptin-associating proteinaceous
CC substance (apoptin-associating protein 1 (AAP-1)), which is capable of
CC inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for
CC inducing a p53-independent apoptosis. They are used for treating a
CC disease where enhanced proliferation or decreased cell death is observed

CC e.g. cancer or autoimmune disease. They are also used for diagnosis of
CC diseases related with aberrations in the apoptotic process such as cancer
CC and autoimmune diseases
XX Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
SQ
Query Match 93.2%; Score 883; DB 4; Length 1131;
Best Local Similarity 97.7%; Pred. No. 6.7e-233;
Matches 903; Conservative 2; Mismatches 18; Indels 1; Gaps 1;
Qy 24 GGAATTCGATCCTCGAGGCCGCGAAGGCCGGAACAGCTGCTGAAGCCTTTAAATGACGA 83
Db 209 GGTTTTGGGATTTGACGCTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGACGA 268
Qy 84 TCTGCCATGTGAGAAAGGCACCTCCACCAGAAAAACCTCGGATCAATTTCTCAGCTGGTGG 143
Db 269 TCTGCCATGTGAGAAAGGCACCTCCACCAGAAAAACCTCGGATCAATTTCTCAGCTGGTGG 328
Qy 144 CNCAACAAGTGGCACAACAGATATGCCACCCACCACCCCTTAAAAAGGAGAGAGAGA 203
Db 329 CACAACAAGTGGCACAACAGATATGCCACCCACCACCCCTTAAAAAGGAGAGAGAGA 388
Qy 204 AAGTTGAAAGCAGGACAAGAGAACCTTGAGAAACCAAGGAAATTTAGTCTTAGTGTGA 263
Db 389 AAGTTGAAAGCAGGACAAGAGAACCTTGAGAAACCAAGGAAATTTAGTCTTAGTGTGA 448
Qy 264 CCAAGAAAAATACCAACAAGAAAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 323
Db 449 CCAGAAAAATACCAACAAGAAAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 508
Qy 324 GTGAAGCAAAACAGCATACTGCTGCAAAATGCTACAAAGAACGACGCAAAACAAATCACA 383
Db 509 GTGAAGCAAAACAGCATACTGCTGCAAAATGCTACAAAGAACGACGCAAAACAAATCACA 568
Qy 384 CCTCAGAGCCCGCTGCAAAACGTCGACAGGAGCACTGCACAGCAGTTCGCGACTACTG 443
Db 569 CCTCAGAGCCCGCTGCAAAACGTCGACAGGAGCACTGCACAGCAGTTCGCGACTACTG 628
Qy 444 TGGGCAACGTCACCGTCATTATCAGACATTTTAAAGGAAAAAGACTCGCTCTCTATCGACAT 503
Db 629 TGGGCAACGTCACCGTCATTATCAGACATTTTAAAGGAAAAAGACTCGCTCTCTATCGACAT 688
Qy 504 CCTCATCCACAGTGACCTCCAGTGCAGGGTTCAGAAACGACGAGAACCCAGACAGCTCGGGGT 563
Db 689 CCTCATCCACAGTGACCTCCAGTGCAGGGTTCAGAAACGACGAGAACCCAGACAGCTCGGGGT 748
Qy 564 CAGAGACACAGACAGAGGGCTCTCCGCTTCCTCCAGCCCAAGGGCGACATGTCAGCAG 623
Db 749 CAGAGACACAGACAGAGGGCTCTCCGCTTCCTCCAGCCCAAGGGCGACATGTCAGCAG 808
Qy 624 TCAATGATGAATCTTTCTGAAATTCACATGGAATTTGAAAACTATGAATTCAGGGGTATG 683
Db 809 TCAATGATGAATCTTTCTGAAATTCACATGGAATTTGAAAACTATGAATTCAGGGGTATG 868
Qy 684 AAATTTCAAAACCTCCACCTCCCATGCTGCTGATCCCTCGAGAAATTTCTTGTGAGACAT 743
Db 869 AAATTTCAAAACCTCCACCTCCCATGCTGCTGATCCCTCGAGAAATTTCTTGTGAGACAT 928
Qy 744 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAAG 803
Db 929 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAAG 988
Qy 804 GAATTTCCGACCCCTGACGATTAATCTTGACACTTTTATGTAATCCATTGTTTATATGAT 863
Db 989 GAATTTCCGACCCCTGACGATTAATCTTGACACTTTTATGTAATCCATTGTTTATATGAT 1048
Qy 864 TTTCTTAAACATCAATTTATATATGATGCTCTGGAATCTACTTTTATATAAAAAAGCC 923
Db 1049 TTTCTTAAACATCAATTTATATATGATGCTCTGGAATCTACTTTTAT-AAAAAGGCC 1107
Qy 924 TTYGTGGCCTCGAGATCTATGA 947
Db 1108 TTCTGGCCTCGAGATCTATGA 1131

RESULT 6	
AAFP57185	
ID	AAFP57185 standard; cDNA; 1131 BP.
XX	
XX	
AC	AAFP57185;
XX	
DT	29-MAY-2001 (first entry)
XX	
DE	Apoptin-associating protein (AAP)-1-b nucleotide sequence.
XX	
KW	Apoptin-associating protein; AAP; apoptosis; p53; cell proliferation;
KW	cell death; cancer; autoimmune disease; cytostatic; immunosuppressive;
KW	gene therapy; AAP-1-b; ss.
XX	
OS	Homo sapiens.
XX	
PH	Location/Qualifiers
FT	76..1131
FT	/*tag= a
FT	/transl_except= (pos:826..828, aa:Xaa)
FT	/transl_except= (pos:937..939, aa:Xaa)
FT	/transl_except= (pos:940..942, aa:Xaa)
FT	/transl_except= (pos:1015..1017, aa:Xaa)
FT	/transl_except= (pos:1045..1047, aa:Xaa)
FT	/transl_except= (pos:1054..1056, aa:Xaa)
FT	/product= "partial AAP-1-b protein"
FT	/note= "Xaa are residues encoded by stop codons"
XX	
PN	EPI083224-A2.
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PD	14-MAR-2001.
XX	
PF	01-SEP-2000; 2000EP-00203042.
XX	
PR	02-SEP-1999; 99EP-00202858.
PR	21-OCT-1999; 99EP-00203465.
XX	
PA	(LEAD-) LEADD BV.
XX	
PI	Noteborn MM, Danen-Van Oorschot AAAM;
XX	
DR	WPI; 2001-228257/24.
DR	P-PSDB; AAB62059.
XX	
PT	New nucleic acids encoding apoptin-associating proteins capable of
PT	inducing p52 independent apoptosis, useful for treating a disease
PT	associated with enhanced cell proliferation or decreased cell death, e.g.
PT	cancer or autoimmune disease.
XX	
PS	Claim 6; Fig 2; 26pp; English.
XX	
CC	The invention provides isolated or recombinant nucleic acid (I), its
CC	functional encoding an apoptin-associating proteinaceous (AAP) substance
CC	capable of apoptosis. (I), the vector comprising (I), the host cell
CC	comprising the vector and the proteinaceous substance encoded by (I) are
CC	useful for inducing apoptosis, particularly p53-independent apoptosis,
CC	and for treating a disease where enhanced cell proliferation or decreased
CC	cell death is observed, such as cancer or an autoimmune disease. A
CC	composition comprising the nucleic acid or the AAP may further be used
CC	for diagnosing a disease related with aberrancies in the apoptotic
CC	process, and for detecting the presence of cancer cells or cells that are
CC	prone to cancer. The present sequence represents the nucleotide sequence
CC	of the AAP-1-b cDNA clone encoding a partial AAP-1-b protein
XX	
SQ	Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
Query Match	93.2%; Score 883; DB 5; Length 1131;
Best Local Similarity	97.7%; Pred. No. 6.7e-233;
Matches	903; Conservative 2; Mismatches 18; Indels 1; Gaps 1;
XX	
XX	24 GGAATTCGGATCCTCGAGGCCACGAAGCGCGAAACAGTGTGAAGCCTTTAAATGCAGCA 83

Db	209	GGTTTGGGATTTGTAGCGTCTGCACCTTCAGAAACAGTCTGAAGCCTTTAAATGCAGCA	268
QY	84	TCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCCTAGCTGGTG	143
Db	269	TCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCCTAGCTGGTG	328
QY	144	CNCAACAAGTGGCAAAACAGTATGCCACCCACACCCCTTAAAGGAGAGAAGGAGA	203
Db	329	CACAAACAGTGGCAAAACAGTATGCCACCCACACCCCTTAAAGGAGAGAAGGAGA	388
QY	204	AGTTTCAAAGCAGGACAAAGAGAACCTTGAGAAAGACAAGGAAATTTAGTCTTAGTGTTA	263
Db	389	AGTTTCAAAGCAGGACAAAGAGAACCTTGAGAAAGACAAGGAAATTTAGTCTTAGTGTTA	448
QY	264	CCAAGAAAAATACCAACAAGAAAAACCAACCAAGAAAGTCTGACATTTCTGAAGATCTCTCTA	323
Db	449	CCAAGAAAAATACCAACAAGAAAAACCAACCAAGAAAGTCTGACATTTCTGAAGATCTCTCTA	508
QY	324	GTGAAGCAAAACAGCATACAGTCTGCAATGCTACAACAAGAACCGGAAACAAATCACA	383
Db	509	GTGAAGCAAAACAGCATACAGTCTGCAATGCTACAACAAGAACCGGAAACAAATCACA	568
QY	384	CCTCAAGGCCCCCGGCTGAAAAACGTGGACAGAGCACTGCACAGCAGTTTGGCAGTAACCTG	443
Db	569	CCTCAAGGCCCCCGGCTGAAAAACGTGGACAGAGCACTGCACAGCAGTTTGGCAGTAACCTG	628
QY	444	TGGGCAACGTCACCGCTCATTATCACAGACTTTAAGGAAAAAGACTCGCTCCTCATCGACAT	503
Db	629	TGGGCAACGTCACCGCTCATTATCACAGACTTTAAGGAAAAAGACTCGCTCCTCATCGACAT	688
QY	504	CCTCATCCACAGTGACCTCAGTGCAGGGTTCAGAACAGCAGAACCCAGCAGCTCGGGGT	563
Db	689	CCTCATCCACAGTGACCTCAGTGCAGGGTTCAGAACAGCAGAACCCAGCAGCTCGGGGT	748
QY	564	CAGAGAGCACAGACAAGGGCTCTCCCGTTCCTCCACGCAAGGGCGACATGTCTAGCAG	623
Db	749	CAGAGAGCACAGACAAGGGCTCTCCCGTTCCTCCACGCAAGGGCGACATGTCTAGCAG	808
QY	624	TCAATGATGAATCTTTCTGAAATTCACATGGAATTTGTGAAACTATGATCAGGGTATG	683
Db	809	TCAATGATGAATCTTTCTGAAATTCACATGGAATTTGTGAAACTATGATCAGGGTATG	868
QY	684	AAATTCAAAACCTCCACCTGCGCCATGCTGTCATCCCTCGGAGATCTTCTGTGGACAT	743
Db	869	AAATTCAAAACCTCCACCTGCGCCATGCTGTCATCCCTCGGAGATCTTCTGTGGACAT	928
QY	744	CGACCTCTTTAGTGTAGTCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAG	803
Db	929	CGACCTCTTTAGTGTAGTCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAG	988
QY	804	GAATTTGCGACCCCTGACGATTAATCTTTGACATTTTATGATTTTATGATTTTATGAT	863
Db	989	GAATTTGCGACCCCTGACGATTAATCTTTGACATTTTATGATTTTATGATTTTATGAT	1048
QY	864	TTTCTTAAACAATTTATTAATTTGATGCTGCTCCTGAAATCTACTTTTATAAAAAAGCC	923
Db	1049	TTTCTTAAACAATTTATTAATTTGATGCTGCTCCTGAAATCTACTTTTAT-AAAAAGGCC	1107
QY	924	TTTGTGGCCCTCGAGAGATCTATGA 947	
Db	1108	TTTGTGGCCCTCGAGAGATCTATGA 1131	

RESULT 7

ACF34480

ID ACF34480 standard; DNA; 1128 BP.

XX ACF34480;

XX ACF34480;

DT 15-OCT-2003 (first entry)

XX

DE Gene encoding angiogenesis protein BNO98.

XX Cystostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antipapillary; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;
KW gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; cardiovascular disease; atherosclerosis;
KW ischemic limb disease; coronary artery disease; gene; ds.
XX
OS Homo sapiens.
XX
XX WO2003027285-A1.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-AU001282.
XX
XX 27-SEP-2001; 2001AU-00007973.
XX
XX 27-SEP-2001; 2001AU-00007974.
XX
XX 11-OCT-2001; 2001AU-00008210.
XX
XX 29-OCT-2001; 2001AU-00008532.
XX
XX 13-NOV-2001; 2001AU-00008938.
XX
XX 28-AUG-2002; 2002AU-00951032.
XX
XX (BION-) BIONOMICS LTD.
XX
XX Gamble JR, Hahn CN, Vadas MA;
XX
XX WPI; 2003-354655/33.
XX
XX P-PSDB; ABR64205.
XX
XX New angiogenic genes and polypeptides, useful for diagnosing,
XX prognosticating or treating an angiogenesis-related disorder, e.g.
XX cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or
XX cardiovascular diseases.
XX
XX Claim 2; SEQ ID NO 35; 90pp; English.
XX
XX The invention relates to the isolation of novel genes (ACF34446-ACF34559)
XX encoding proteins (ABR64180-ABR64281) involved in the process of
XX angiogenesis. The nucleic acid molecules are useful in identifying and/or
XX obtaining full-length human genes involved in an angiogenic process. The
XX nucleic acid molecule, polypeptides or complexes encoded, cells or
XX genetically modified non-human animals derived from these are useful for
XX the screening of candidate pharmaceutical compounds used in treating
XX angiogenesis-related disorders. They are also useful for diagnosing,
XX prognosticating or treating an angiogenesis-related disorder, which
XX involves uncontrolled or enhanced angiogenesis or is a disorder in which
XX a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,
XX diabetic retinopathy, psoriasis or cardiovascular diseases such as
XX atherosclerosis), or involves inappropriately arrested or decreased
XX angiogenesis or is a disorder in which an expanding vasculature is of
XX benefit (e.g. ischemic limb disease or coronary artery disease). The
XX modulator of expression or activity of the polypeptide encoded by the
XX nucleic acid sequence is useful for manufacturing a medicament for the
XX treatment of an angiogenesis-related disorder. This sequence corresponds
XX to the gene encoding one of the novel angiogenic protein
XX
XX Sequence 1128 BP; 341 A; 230 C; 282 G; 215 T; 0 U; 0 Other;
XX
XX Query Match 91.9%; Score 870; DB 8; Length 1128;
XX Best Local Similarity 98.0%; Pred. NO. 2.6e-229;
XX Matches 879; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
XX
XX 24 GGAATTCGGATTCGAGCCACGAGCGCCGGAACAGTCTGAGCCCTTTAAATGCAGCA 83
XX
XX 219 GGTTTGGGATGTGACGCTCTGCACCTTCAGAAACAGTGTGAGCCCTTTAAATGCAGCA 278
XX
XX 84 TCTGGATGTGAGGAAGGACCTCCACAGAAAACCTCGGATCAATTTCTCAGCTGGTGG 143
XX
XX 279 TCTGGATGTGAGGAAGGACCTCCACAGAAAACCTCGGATCAATTTCTCAGCTGGTGG 338
XX
XX 144 CACAAAGTGGCAACAGTATGCCACCCACCAACCCCTTAAAGAGGAGGAGA 203
XX
XX 339 CGCAACAGTGGCAACAGTATGCCACCCACCAACCCCTTAAAGAGGAGGAGA 398
XX

QY 204 AAGTTGAAAGCAGGACAAAGAGAAAACCTTGAGAAAGACAAAGAAATTAGTCTAGTGTTA 263
DB 399 AAGTTGAAAGCAGGACAAAGAGAAAACCTTGAGAAAGACAAAGAAATTAGTCTAGTGTTA 458
QY 264 CCAAGAAAATACCAACAGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 323
DB 459 CCAAGAAAATACCAACAGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 518
QY 324 GTCAAGCAACAGCAGATACAGTCTGCAAAATGCTACAAACAAAGACCAAGCAACCAACCAACCA 383
DB 519 GTCAAGCAACAGCAGATACAGTCTGCAAAATGCTACAAACAAAGACCAAGCAACCAACCAACCA 578
QY 384 CTTCAAGGCCCGGCTGAAAAACGTTGGACAGAGGACCTGACACAGCAGTTGGCAGTAACCTG 443
DB 579 CTTCAAGGCCCGGCTGAAAAACGTTGGACAGAGGACCTGACACAGCAGTTGGCAGTAACCTG 638
QY 444 TGGGCAACGTCACCGTCATTTACACAGACTTTTAAAGCAAAAGAGCTCGCTCTCATCGACAT 503
DB 639 TGGGCAACGTCACCGTCATTTACACAGACTTTTAAAGCAAAAGAGCTCGCTCTCATCGACAT 698
QY 504 CTTCAATCCACAGTGACCTCCAGTGCAGGGTCCAGAAACAGCAGCAACCAAGCAGCTCGGGGT 563
DB 699 CTTCAATCCACAGTGACCTCCAGTGCAGGGTCCAGAAACAGCAGCAACCAAGCAGCTCGGGGT 758
QY 564 CAGAGAGCAGACAAAGGGCTCTCCCGTTCTCCAGCGCCAAAGGGGCGACATGTCAGCAG 623
DB 759 CAGAGAGCAGACAAAGGGCTCTCCCGTTCTCCAGCGCCAAAGGGGCGACATGTCAGCAG 818
QY 624 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGTAAGAACTATGAATCAGGGTATG 683
DB 819 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGTAAGAACTATGAATCAGGGTATG 878
QY 684 AAATTCAAAACCTCCACCTGCGCATCTGCTGATCCCTCGAGAACTCTTCTGTGGACAT 743
DB 879 AAATTCAAAACCTCCACCTGCGCATCTGCTGATCCCTCGAGAACTCTTCTGTGGACAT 938
QY 744 CGACCTCTTAGTGATGTCGACGAGTAATTTCTGCTGCAATGGGCAATCTGGCCACCAAG 803
DB 939 CGACCTCTTAGTGATGTCGACGAGTAATTTCTGCTGCAATGGGCAATCTGGCCACCAAG 998
QY 804 GAATTTGGACCCCTGAGGATTAATCTTGACACTTTTATGTTATGTTTATGAT 863
DB 999 GAATTTGGACCCCTGAGGATTAATCTTGACACTTTTATGTTATGTTTATGAT 1058
QY 864 TTTCTCAACCAATATTATTAATTTGGATGCTCTGCTGAATCTACTTTTATATAAAAAA 920
DB 1059 TTTCTCAACCAATATTATTAATTTGGATGCTCTGCTGAATCTACTTTTATATAAAAAA 1115
XX
XX RESULT 8
XX AAZ52452
XX ID AAZ52452 standard; DNA; 3641 BP.
XX AC
XX AAZ52452;
XX
XX 24-FEB-2000 (first entry)
XX
XX HTRM clone 3149729 DNA sequence.
XX
XX HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS;
XX arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; ss;
XX Addison's disease; multiple sclerosis; rheumatoid arthritis; infection;
XX trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
XX
XX Homo sapiens.
XX
XX WO9957144-A2.
XX
XX 11-NOV-1999.
XX
XX 04-MAY-1999; 99WO-US009935.
XX
XX

CC The invention relates to an inhibitory RNA (RNAi) molecule derived from a
CC nucleic acid molecule comprising a defined nucleic acid sequences given
CC in the specification or a sequence which hybridizes to the sequences and
CC encodes a Notch signaling target gene or which is a degenerate as a
CC result of the genetic code of the sequences. The methods and compositions
CC of the present invention are useful for manipulating the phenotype of
CC stem cells, preferably pluripotent stem cells. This sequence corresponds
CC to one of the nucleic acid molecules of the invention.
XX
XX
SQ Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;

Query Match 91.7%; Score 868.4; DB 10; Length 1036;
Best Local Similarity 97.9%; Pred. No. 6.8e-229;
Matches 878; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

Qy 24 GGAATTCGGATCCTCGAGGCCACGAGCCGAAACAGTGTCTGAAGCCCTTTAAATGCAGCA 83
Db 135 GGTTTTGGATTTAGCGTCTGCACTTCAGAAACAGTGTCTGAAGCCCTTTAAATGCAGCA 194

Qy 84 TCTCGATGTGAGGAAGGCACTCCACGAAACCTCGGATCAATTTCTCAGCTGGTGG 143
Db 195 TCTCGATGTGAGGAAGGCACTCCACGAAACCTCGGATCAATTTCTCAGCTGGTGG 254

Qy 144 CNCAACAAAGTGGCAACAGTATGCCACCCACCCACCCCTTAAAGAGGAAGGAGA 203
Db 255 CACAACAAAGTGGCAACAGTATGCCACCCACCCCTTAAAGAGGAAGGAGA 314

Qy 204 AAGTTGAAAGCAGGACAAAGAGAACTGTGAAAGCAAGGAAATAGTCTAGTGTGA 263
Db 315 AAGTTGAAAGCAGGACAAAGAGAACTGTGAAAGCAAGGAAATAGTCTAGTGTGA 374

Qy 264 CCAGAGAAATACCAACAAAGAAACCAAACTGACATCTGAAAGATCCTCTTA 323
Db 375 CCAGAGAAATACCAACAAAGAAACCAAACTGACATCTGAAAGATCCTCTTA 434

Qy 324 GTGAAGCAAAACAGCATACAGTCTGCAATGTCTACAAAGAACCCAGCGGAAACAAATCACA 383
Db 435 GTGAAGCAAAACAGCATACAGTCTGCAATGTCTACAAAGAACCCAGCGGAAACAAATCACA 494

Qy 384 CCTAAGCCCGGCTGAAAAACGTGGACAGGACCTGCAAGAGTGGCAGTACTG 443
Db 495 CCTAAGCCCGGCTGAAAAACGTGGACAGGACCTGCAAGAGTGGCAGTACTG 554

Qy 444 TGGGCAAGCTCACCGTCAATATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACAT 503
Db 555 TGGGCAAGCTCACCGTCAATATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACAT 614

Qy 504 CCTCATCCACAGTGAACCTCCAGTGCAGGGTTCAGAACAGACAGACAGTCTGGGGT 563
Db 615 CCTCATCCACAGTGAACCTCCAGTGCAGGGTTCAGAACAGACAGACAGTCTGGGGT 674

Qy 564 CAGAGACACAGCAAGGGCTCTCCCGTTCTCCAGCCAAAGGGCGACATGTCAGCAG 623
Db 675 CAGAGACACAGCAAGGGCTCTCCCGTTCTCCAGCCAAAGGGCGACATGTCAGCAG 734

Qy 624 TCAATGATGAATCTTCTGAAATTCACATGGAATTTGAAACCTATCAATCAGGATG 683
Db 735 TCAATGATGAATCTTCTGAAATTCACATGGAATTTGAAACCTATCAATCAGGATG 794

Qy 684 AAATTCAAAACCTCCACCTGCCCAGTCTGCTTGCATCCCTGGAGAACTCTCTGTGGACAT 743
Db 795 AAATTCAAAACCTCCACCTGCCCAGTCTGCTTGCATCCCTGGAGAACTCTCTGTGGACAT 854

Qy 744 CGACCTCTTAGTGTGTCGCAAGGATAATTTCTGCTGGCATGCGCATCTGGCCACCAAG 803
Db 855 CGACCTCTTAGTGTGTCGCAAGGATAATTTCTGCTGGCATGCGCATCTGGCCACCAAG 914

Qy 804 GAAATTCGACCCCTGACGATTTACTCTTGACACTTTTATGTTATGTTTATATCAT 863
Db 915 GAAATTCGACCCCTGACGATTTACTCTTGACACTTTTATGTTATGTTTATATCAT 974

Qy 864 TTTCTTAAACATCATTTAATTTGATGTGCTCTCGAATCTACTTTTTTATAAAAA 920

Db 975 TTTCCTAACAAATCATTTATAATTTGGATGTGCTCCTGAAATCTACTTTTATAAAAAA 1031

RESULT 10
ADK61399
ID ADK61399 standard; DNA; 1036 BP.
XX AC
XX ADK61399;
XX
DT 06-MAY-2004 (first entry)
XX
XX Ovarian cancer-related DNA #554 with altered ovarian cancer expression.
XX ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
KW gene expression; primer; cancer.
XX Homo sapiens.
XX OS
XX WO2003068054-A2.
XX PN
XX 21-AUG-2003.
XX PD
XX 13-FEB-2003; 2003WO-US004688.
XX PF
XX 13-FEB-2002; 2002US-0357031P.
XX PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Jazaeri AA, Boyd J, Liu ET;
XX WPI; 2003-689589/65.
XX DR
XX
XX Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
PT like tumor by determining a pattern of expression in the ovarian tumor of
PT several markers.
XX
XX Disclosure; SEQ ID NO 569; 137pp; English.
XX
XX The invention relates to a method of classifying an ovarian tumor as a
CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;

Query Match 91.7%; Score 868.4; DB 10; Length 1036;
Best Local Similarity 97.9%; Pred. No. 6.8e-229;
Matches 878; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

Qy 24 GGAATTCGGATCCTCGAGGCCACGAGCCGAAACAGTGTCTGAAGCCCTTTAAATGCAGCA 83
Db 135 GGTTTTGGATTTAGCGTCTGCACTTCAGAAACAGTGTCTGAAGCCCTTTAAATGCAGCA 194

Qy 84 TCTCGATGTGAGGAAGGCACTCCACGAAACCTCGGATCAATTTCTCAGCTGGTGG 143
Db 195 TCTCGATGTGAGGAAGGCACTCCACGAAACCTCGGATCAATTTCTCAGCTGGTGG 254

Qy 144 CNCAACAAAGTGGCAACAGTATGCCACCCACCCACCCCTTAAAGAGGAAGGAGA 203
Db 255 CACAACAAAGTGGCAACAGTATGCCACCCACCCCTTAAAGAGGAAGGAGA 314

Qy 204 AAGTTGAAAGCAGGACAAAGAGAACTGTGAAAGCAAGGAAATAGTCTAGTGTGA 263

Db 315 AAGTTGAAGACGAGCAAGAGAGAACTCTGAGAAAGACAGGAAATTTAGTCCTAGTGTTA 374
Qy 264 CCAAGAAAAATACCAACAGAAAAACCAAAACCAAAAGTCTGACATTTCTGAAAGATCCTCCTA 323
Db 375 CCAAGAAAAATACCAACAGAAAAACCAAAACCAAAAGTCTGACATTTCTGAAAGATCCTCCTA 434
Qy 324 GTGAAGCAACAGACATACAGTCTGCAATCTCAATCTCAACAGAAAGCCAGGAAACCAATCACA 383
Db 435 GTGAAGCAACAGACATACAGTCTGCAATCTCAATCTCAACAGAAAGCCAGGAAACCAATCACA 494
Qy 384 CCTCAAGCCCGCGCTGAAAAACCTGGACAGGAGCACTGCACAGCAGCTTGGCAGTAACTG 443
Db 495 CCTCAAGCCCGCGCTGAAAAACCTGGACAGGAGCACTGCACAGCAGCTTGGCAGTAACTG 554
Qy 444 TGGCAACAGTCACCGCTCATTTATCAGACTTTAAGGAAAAAGACTCGCTCTCTCATCGACAT 503
Db 555 TGGCAACAGTCACCGCTCATTTATCAGACTTTAAGGAAAAAGACTCGCTCTCTCATCGACAT 614
Qy 504 CCTCATCCAGTCAGCTCCAGTGCAGGCTCAGAAACAGCAGCAACCCAGCAGCTCGGGGT 563
Db 615 CCTCATCCAGTCAGCTCCAGTGCAGGCTCAGAAACAGCAGCAACCCAGCAGCTCGGGGT 674
Qy 564 CAGAGACACAGACAAGGGCTCTCCCGTTCTCCAGCCGCAAGGGCGGACATGTTCAGCAG 623
Db 675 CAGAGACACAGACAAGGGCTCTCCCGTTCTCCAGCCGCAAGGGCGGACATGTTCAGCAG 734
Qy 624 TCAATGATGAATCTTTCTGAAATTCGACATGGAATTTGGAATTCGAAATTCGAGGTATG 683
Db 735 TCAATGATGAATCTTTCTGAAATTCGACATGGAATTTGGAATTCGAAATTCGAGGTATG 794
Qy 684 AAATTTCAAAACCTCCAGCTCCAGTCTGCTGTCATCCCTGGAGAACTCTCTGAGACAT 743
Db 795 AAATTTCAAAACCTCCAGCTCCAGTCTGCTGTCATCCCTGGAGAACTCTCTGAGACAT 854
Qy 744 CGACCTCTTAGTGATGCTGCAGAGTAATTTCTGCTTGGCATGGGCATCTGGCCACCAAG 803
Db 855 CGACCTCTTAGTGATGCTGCAGAGTAATTTCTGCTTGGCATGGGCATCTGGCCACCAAG 914
Qy 804 GAATTTGCGACCTTCGACATTAATCTCTTGACACTTTTATGATTCATTTTATATGAT 863
Db 915 GAATTTGCGACCTTCGACATTAATCTCTTGACACTTTTATGATTCATTTTATATGAT 974
Qy 864 TTTCTCAACATCATTTTATATGATGCTGCTCTGCTGATCTACTTTTTTATAAAAAA 920
Db 975 TTTCTCAACATCATTTTATATGATGCTGCTCTGCTGATCTACTTTTTTATAAAAAA 1031

RESULT 11
ADD18793
ID ADD18793 standard; DNA; 4700 BP.
XX AC
AC ADD18793;
XX AC
DT 15-JAN-2004 (first entry)
XX DE
DE Human disease related protein DNA sequence SeqID224.
XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnery; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemia; condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing; gene; ds.
XX
OS Homo sapiens.
XX
FN WO2003018621-A2.
XX
PD 06-MAR-2003.
XX
XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.
PR 05-OCT-2001; 2001GB-00024037.
XX
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingeman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX
DR WPI; 2003-290046/28.
DR P-PSDB; ADD18792.
XX
XX New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX
XX Claim 27; SEQ ID NO 224; 424pp; English.
PS
PS This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory, the
CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX
SQ Sequence 4700 BP; 1411 A; 898 C; 942 G; 1446 T; 0 U; 3 Other;
Query Match 91.5%; Score 866.8; DB 10; Length 4700;
Best Local Similarity 97.8%; Pred. No. 3.9e-228;
Matches 877; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
Qy 24 GGAATTCGATCTCGAGGCCAGAGGCGGAAACAGTCTGAAGCCTTTAAATGACGA 83
Db 260 GGTGTTGGGATTTAGCGTCTGCACCTTCAGAAACAGTCTGAAGCCTTTAAATGACGA 319
Qy 84 TCTGCCATGTGAGGAAGGCACCTCCACAGAAACCTCGATCAATTTCTCAGCTGTTG 143
Db 320 TCTGCCATGTGAGGAAGGCACCTCCACAGAAACCTCGATCAATTTCTCAGCTGTTG 379
Qy 144 CNCAACAAGTGGCACAACAGATATGCCACCCCTCACCCCTTAAAAAGGAGAAGAGGA 203
Db 380 CACAACAAGTGGCACAACAGATATGCCACCCCTCACCCCTTAAAAAGGAGAAGAGGA 439
Qy 204 AGTTGAAAGCAGGACAAAGAAACCTTGAGAAAGACAGGAATTAGTCTTAGTGTTA 263
Db 440 AAGTTGAAAGCAGGACAAAGAAACCTTGAGAAAGACAGGAATTAGTCTTAGTGTTA 499
Qy 264 CCAAGAAAATACCAACAGAAACCAACACCAAGTCTGACATTTCTGAAAGATCCTCCTA 323
Db 500 CCAAGAAAATACCAACAGAAACCAACACCAAGTCTGACATTTCTGAAAGATCCTCCTA 559
Qy 324 GTGAAGCAACAGACATACAGTCTGCAATCTCAACAGAAAGCCAGGAAACCAATCACA 383
Db 560 GTGAAGCAACAGACATACAGTCTGCAATCTCAACAGAAAGCCAGGAAACCAATCACA 619
Qy 384 CCTCAAGCCCGCGCTGAAAAACCTGGAGCAGGAGCACTGCACAGCAGTGTGGAGTAACTG 443
Db 620 CCTCAAGCCCGCGCTGAAAAACCTGGAGCAGGAGCACTGCACAGCAGTGTGGAGTAACTG 679
Qy 444 TGGGCAACCTCAACCGCTCATTTATCAGACTTTAAGGAAAAAGACTCGCTCTCTCATCGACAT 503
Db 680 TGGGCAACCTCAACCGCTCATTTATCAGACTTTAAGGAAAAAGACTCGCTCTCTCATCGACAT 739
Qy 504 CCTCATCCAGTCAGCTCCAGTGCAGGCTCAGAAACAGCAGCAACCCAGCAGCTCGGGGT 563

Db 740 CCTCATCCACAGTGAACCTCCAGTGCAGGGTCCGAACAGCAGAACCCAGCAGCAGCTCGGGT 799
Qy 564 CAGAGACACAGACAAGGGCTCCCTCCGTTCTCCAGCCCAAGGGGCGACATCTCAGCAG 623
Db 800 CTGAGACACAGACAAGGGCTCCCTCCGTTCTCCAGCCCAAGGGGCGACATCTCAGCAG 859
Qy 624 TCAATGATGAATCTTCTGAAATTCACATGGAATTCGAAACTATGAATCAGGGTATG 683
Db 860 TCAATGATGAATCTTCTGAAATTCACATGGAATTCGAAACTATGAATCAGGGTATG 919
Qy 684 AAATTCAAAACCTCCACCTGCCCATGCTGTTCATCCCTGGAGAACTCTTCGTGGACAT 743
Db 920 AAATTCAAAACCTCCACCTGCCCATGCTGTTCATCCCTGGAGAACTCTTCGTGGACAT 979
Qy 744 CGACCTCTTAGTGTGTCGACAGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG 803
Db 980 CGACCTCTTAGTGTGTCGACAGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG 1039
Qy 804 GAATTCGCACCCCTGACGATTACTCTTGACACTTTTATGTTATTCATTGTTTATATGAT 863
Db 1040 GAATTCGCACCCCTGACGATTACTCTTGACACTTTTATGTTATTCATTGTTTATATGAT 1099
Qy 864 TTTCCTAACAACTAATTTATTAATTCGATGTGCTCTCGAATCTACTTTTTATAAAAAA 920
Db 1100 TTTCCTAACAACTAATTTATTAATTCGATGTGCTCTCGAATCTACTTTTTATAAAAAA 1156

RESULT 12
AAS34877
ID AAS34877 standard; cDNA; 2156 BP.
AC AAS34877;
XX
XX
DT 04-DEC-2001 (first entry)
XX
XX
DE cDNA encoding novel human neoplastic disease associated polypeptide #111.
XX
KW Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
OS Homo sapiens.
XX
XX WO200155163-A1.
XX
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001358.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465558/50.
XX P-PSDB; AAU21678.
XX
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to
XX diagnose diseases or disorders associated with aberrant expression or
XX activity of polypeptides, and for treating cancers, rheumatoid arthritis.
XX
XX Claim 4; SEQ ID NO 121; 687pp; English.
XX
XX The present invention relates to the isolation of novel human neoplastic
XX disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA
XX sequences encoding for these polypeptides. The sequences of the invention
XX are useful in the diagnosis, treatment, prevention and/or prognosis of
XX disorders involving neoplastic disease such as hyperproliferative
XX disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem
XX glioma, adult liver cancer, childhood cerebellar astrocytoma, or
XX Hodgkin's lymphoma). The sequences of the invention may also be useful
XX for treating other disorders such as neural disorders, immune system
XX disorders, muscular disorders, reproductive disorders, gastrointestinal
XX disorders, pulmonary disorders, cardiovascular disorders and renal
XX disorders. The polynucleotide sequences of the invention are also useful
XX in gene therapy. AAS34767-AAS35050 represent cDNA sequences encoding for
XX the novel human neoplastic disease associated polypeptides of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_sequences

SQ Sequence 2156 BP; 659 A; 465 C; 419 G; 613 T; 0 U; 0 Other;
Query Match 90.7%; Score 859; DB 4; Length 2156;
Best Local Similarity 97.9%; Pred. No. 3.8e-226;
Matches 879; Conservative 1; Mismatches 17; Indels 1; Gaps 1;
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DB 64 GGTTCGGATTCGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCTTTTAAATGCAGCA 123
QY 84 TCTGCGATGTGAGGAAAGGCACCTCCACCA -GAAAACTCTGGATCAATTTCTAGCTGGTG 142
DB 124 TCTGCGATGTGAGGAAAGGCACCTCCACCATGAAAACCTCGGATCAATTTCTAGCTGGTG 183
QY 143 GNCACCAAGTGGCACAAACAGTATGCCACCCACACCCCTTAAAGGAGGAGGAG 202
DB 184 GCACACCAAGTGGCACAAACAGTATGCCACCCACACCCCTTAAAGGAGGAGGAG 243
QY 203 AAGTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 262
DB 244 AAGTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
QY 263 ACCAAGAAAAATACCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 322
DB 304 ACCAAGAAAAATACCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
QY 323 AGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 382
DB 364 AGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 423
QY 383 ACCTCAAGGCCCGGCTGAAAACGTTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 442
DB 424 ACCTCAAGGCCCGGCTGAAAACGTTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 483
QY 443 GTGGCAACGTCACCGTCATTATCACAGACTTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 502
DB 484 GTGGCAACGTCACCGTCATTATCACAGACTTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 543
QY 503 TCCTCATCCAGTGCACCTCCAGTGCAGGTCAGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 562
DB 544 TCCTCATCCAGTGCACCTCCAGTGCAGGTCAGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 603
QY 563 TCAGAGAGCACAGACAAAGGCTCTCCCGTTCTCCACGCGCAAGGCGGAGCATGTGCAGCA 622
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QY 623 GTCAATGATGAATCTTTTCTGAAATTCACATGGAATTTGTGAAACTATGAAATCAGGGTAT 682
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QY 683 GAAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCCCTGGAGAACTCTTCTGTGGACA 742
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QY 803 GGAATTTGCGCACCTCCAGATTAATCTTGCACATTTTATGATATTCATGTTTTATATGA 862
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ID ADC46035 standard; cDNA; 2156 BP.
XX
XX AC
XX ADC46035;

DT 18-DEC-2003 (first entry)
XX Human neoplastic disease-associated gene 111 cDNA #1.
DE
XX
XX
KW Neoplastic disease-associated polypeptide; gene therapy;
KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW autoimmune thyroiditis; hemolytic anaemia; haematopoietic disorder;
KW haematologic disorder; anaemia; thrombocytopaenia; allergic reaction;
KW asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; renal disorder;
KW acute glomerulonephritis; end-stage renal disease;
KW cardiovascular disorder; atherosclerosis; myocarditis;
KW infectious disease; AIDS; cachexia; anorexia; wound healing;
KW epithelial cell proliferation; Human; ss.
XX
XX Homo sapiens.
XX
XX US2003082758-A1.
XX
XX 01-MAY-2003.
XX
XX 22-MAR-2002; 2002US-00103313.
XX
XX 31-JAN-2000; 2000US-0179065P.
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
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PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-0076485A.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2003-786918/74.
DR P-PSDB; ADC46319.
XX
XX New isolated human neoplastic disease-associated polypeptides and
PT polynucleotides, useful for diagnosing, preventing, prognosticating or
PT treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
PT disease.
XX
XX Claim 1; SEQ ID NO 121; 302pp; English.
XX
XX The invention relates to one of 238 disclosed human neoplastic disease-
CC associated polypeptides encoded by 171 disclosed cDNA sequences
CC (including their domains, epitopes, full-length proteins, allelic variants
CC or species homologues). Also included are there encoding nucleic acids, a
CC recombinant vector comprising the nucleic acid, a recombinant host cell
CC comprising the nucleic acid (expressing the protein), an isolated
CC antibody that binds specifically to the isolated polypeptide, preventing,
CC treating or ameliorating a medical condition, diagnosing a pathological
CC condition or a susceptibility to a pathological condition in a subject,
CC identifying a binding partner to the polypeptide, identifying an activity
CC in a biological assay, and the gene corresponding to the cDNA sequence.
CC The polypeptides, polynucleotides and antibodies are useful for
CC detecting, preventing, diagnosing, prognosticating, treating or
CC ameliorating medical conditions such as hyperproliferative diseases or
CC cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
CC systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
CC or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
CC anaemia or thrombocytopaenia), allergic reactions including asthma or
CC eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
Query Match 90.7%; Score 859; DB 10; Length 2156;
Best Local Similarity 97.9%; Pred. No. 3.8e-226;
Matches 879; Conservative 1; Mismatches 17; Indels 1; Gaps 1;
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DB 64 GGTTTGGGATGTAGCGTCTGCACCTTCAGAACAGTGTGAGCCCTTTAAATGCGACA 123
QY 84 TCTCGGATGTGAGGAAGGACCTCCACCA-AAAACTCGGATCAATTTCTCAGCTGGTG 142
DB 124 TCTCGGATGTGAGGAAGGACCTCCACCATGAAACCTCGGATCAATTTCTCAGCTGGTG 183
QY 143 GCNCAACAAGTGGCACCAACAGTATGCCCCACCCACCCCTTAAAAAGGAGAAAGGAG 202
DB 184 GCACAACAAGTGGCACCAACAGTATGCCCCACCCACCCCTTAAAAAGGAGAAAGGAG 243
QY 203 AAAGTTGAAAGCGGCAAGAGAAACCTTGAGAAACAAGNAATAGTCTAGTGT 262
DB 244 AAAGTTGAAAGCGGCAAGAGAAACCTTGAGAAACAAGGAAATAGTCTAGTGT 303
QY 263 ACCAAGAAAAATACCAACAAGAAAAACCAAGTCTGACATTTCTGAAAGATCCCTCCT 322

DB 304 ACCAAGAAAAATACCAACAAGAAAAACCAAAAGTCTGACATTTCTGAAAGATCCCTCCT 363
QY 323 AGTGAAGCAAAACAGCATACAGTCTGCAATGCTTACAAACAAGACCAAGCAAAACAAATCAC 382
DB 364 AGTGAAGCAAAACAGCATACAGTCTGCAATGCTTACAAACAAGACCAAGCAAAACAAATCAC 423
QY 383 ACCTCAAGGCCCGGCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACT 442
DB 424 ACCTCAAGGCCCGGCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACT 483
QY 443 GTGGCAACGCTCAACCGTCAATATACAGACTTTTAAGAAAAAGACTCGCTCCTCATCGACA 502
DB 484 GTGGCAACGCTCAACCGTCAATATACAGACTTTTAAGAAAAAGACTCGCTCCTCATCGACA 543
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QY 563 TCAGAGAGCACAGACAAAGGGCTCCTCCGTTCTCCACGCCAAAGGGCGACATGTGACGA 622
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QY 623 GTCAATGATGAATCTTTCTGAAAAATTCACATGGAATTTGAAAAATATGAAATCAGGGTAT 682
DB 664 GTCAATGATGAATCTTTCTGAAAAATTCACATGGAATTTGAAAAATATGAAATCAGGGTAT 723
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DB 724 GAAATTCAAAACCTCCACCTGCCCATGCTGTGCAATCCCTGGAGAAATCTTCTGTGACGA 783
QY 743 TCAGACCTTTAGTGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAA 802
DB 784 TCAGACCTTTAGTGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAA 843
QY 803 GGAATTCGCACCCCTCAGCATTACTCTTGACACTTTTATGATATTCATTGTTTATATGA 862
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QY 863 TTTTCTTAACATCATTATTAATGATGCTGCTCCTGAAATCTTCTTATATAAAAAA 920
DB 904 TTTTCTTAACATCATTATTAATGATGCTGCTCCTGAAATCTTCTTATATAAAAAA 961
RESULT 14
ACH37647
ID ACH37647 standard; cDNA; 502 BP.
XX
XX ACH37647;
AC
XX
DT 13-OCT-2003 (first entry)
XX
DE Human endothelial cell cDNA #5780.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
OS
PN US2003073623-A1.
XX
XX 17-APR-2003.
PD
XX
PF 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
PR
XX
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful

PT as hybridization probes, as oligomers for PCR, for chromosome and gene

PT mapping, in the recombinant production of protein, or in generating

PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 24859; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of

CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was

CC determined by the technique of SH (sequencing by hybridisation). Also

CC included is a purified polypeptide comprising a sequence corresponding to

CC a reading frame of the novel polynucleotide. The nucleic acid sequences

CC are useful in diagnostics as expressed sequence tags (EST) for

CC identifying expressed genes or for physical mapping of the human genome,

CC in forensics, in assessing biodiversity, or in identifying mutations

CC responsible for genetic disorders and other traits. The nucleotide

CC sequences are also useful as hybridisation probes, as oligomers for PCR,

CC for chromosome and gene mapping, in the recombinant production of

CC protein, or in generating antisense DNA or RNA. The purified polypeptide

CC is useful for generating antibodies specific for it. The present sequence

CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data

CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?docID=20030073623

XX

SQ Sequence 502 BP; 138 A; 140 C; 118 G; 105 T; 0 U; 1 Other;

Query Match 49.6%; Score 469.6; DB 9; Length 502;

Best Local Similarity 96.6%; Pred. No. 5.4e-119;

Matches 478; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 337 CATACAGTCTGCAATGCTACAAAGACAGCAGGAAACAAATCACACCTCAAGGCCCG 396

Db 8 CNAATAGATCGTATAGCGGCTCGAGGACGAGGAAACAAATCACACCTCAAGGCCCG 67

Qy 397 GCTGAAAACGTGACAGGACATGTCACAGCTGCGTCTCATCGACATCCTCATCCACAGT 456

Db 68 GCTGAAAACGTGACAGGACATGTCACAGCTGCGTCTCATCGACATCCTCATCCACAGT 127

Qy 457 GGTCAATATACAGACTTTAAGGAAAGACTGCGTCTCATCGACATCCTCATCCACAGT 516

Db 128 GGTCAATATACAGACTTTAAGGAAAGACTGCGTCTCATCGACATCCTCATCCACAGT 187

Qy 517 GACCTCCAGTGCAGGTCAGAACAGCAGAACACAGCAGCTCGGGGTCAGAGACAGAGA 576

Db 188 GACCTCCAGTGCAGGTCAGAACAGCAGAACACAGCAGCTCGGGGTCAGAGACAGAGA 247

Qy 577 CAAGGGCTCTCCGTTCTCTCAGCCGAAAGGGGCGACATGTCAGCAGTCAATGATGATC 636

Db 248 CAAGGGCTCTCTCCGTTCTCTCAGCCGAAAGGGGCGACATGTCAGCAGTCAATGATGATC 307

Qy 637 TTTCTGAAATGTCATGGAATTTGAAATCTATGAAATCAGGGTATGAAATTTCAAACCT 696

Db 308 TTTCTGAAATGTCATGGAATTTGAAATCTATGAAATCAGGGTATGAAATTTCAAACCT 367

Qy 697 CCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGTG 756

Db 368 CCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGTG 427

Qy 757 ATGCTGCCAGGATTAATTTCTGCTTGGCATCTGGCATCTGGCCACCAAGGAATTTGCCACCC 816

Db 428 ATGCTGCCAGGATTAATTTCTGCTTGGCATCTGGCATCTGGCCACCAAGGAATTTGCCACCC 487

Qy 817 TGACGATTAATCTTG 831

Db 488 TGACGATTAATCTTG 502

RESULT 15

RAI14743/C

RAI14743 standard; DNA; 429 BP.

AAI14743;

12-OCT-2001 (first entry)

Probe #4676 for gene expression analysis in human cervical cell sample.

Probe; human; microarray; gene expression; cervical epithelial cell;

cervical cancer; ss.

Homo sapiens.

MO200157278-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US000670.

04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

(MOLB-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488901/53.

Human genome-derived single exon nucleic acid probes useful for analyzing

gene expression in human cervical epithelial cells.

Claim 25; SEQ ID NO 4676; 487pp; English.

The present invention relates to human single exon nucleic acid probes

(SENPs). The present sequence is one such probe. The SENPs are derived

from human HeLa cells. The SENPs can be used to produce a single exon

microarray, which can be used for measuring human gene expression in a

sample derived from human cervical epithelial cells. By measuring gene

expression, the probes are therefore useful in grading and/or staging of

diseases of the cervix, notably cervical cancer. Note: The sequence data

for this patent did not form part of the printed specification, but was

obtained in electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences

Sequence 429 BP; 94 A; 99 C; 117 G; 119 T; 0 U; 0 Other;

Query Match 45.3%; Score 428.6; DB 4; Length 429;

Best Local Similarity 99.8%; Pred. No. 1e-107;

Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 401 AAAAACTGACAGGAGCACTGCACAGCAGTTCGCGACTTAACCTGCGGCAACGTCACCGTC 460

Db 429 AAAAACTGACAGGAGCACTGCACAGCAGTTCGCGACTTAACCTGCGGCAACGTCACCGTC 370

Qy 461 ATTATACACAGCTTTAAGGAAAAAGACTCGCTCTCATCGACATCCTCATCCAGTGCACC 520

Db 369 ATTATACACAGCTTTAAGGAAAAAGACTCGCTCTCATCGACATCCTCATCCAGTGCACC 310

Qy 521 TCCAGTCAGGGTCAGAACAGCAGAACACAGCAGCTCGGGGTCAGAGAGCAGACAGCAAG 580

Db 309 TCCAGTCAGGGTCAGAACAGCAGAACACAGCAGCTCGGGGTCAGAGAGCAGACAGCAAG 250

Qy 581 GGCTCTCTCCGTTCTCTCCAGGCCAAAGGGGCGACATGTGACAGTCAATGATGATCTTTC 640

Db 249 GGCTCTCTCCGTTCTCTCCAGGCCAAAGGGGCGACATGTGACAGTCAATGATGATCTTTC 190

Qy 641 TGAATTTGCAATGGAATTTGAAAACTATGAAATCAGGGTATGAAATTTCAAACCTCCAC 700

Db	189	TGAAATTGCACATGGAATTGTGAAACTATGAATCAGGGTATGAAATTCAAAACTCCAC	130
Qy	701	CTGCCCATGCTGCTTGCATCCCTGGAGAACTTTCTGTGGACATCGACCTCTTAGTGATGC	760
Db	129	CTGCCCATGCTGCTTGCATCCCTGGAGAACTTTCTGTGGACATCGACCTCTTAGTGATGC	70
Qy	761	TGCCAGGATAATTTCTGCTTGGCCATGGGCATCTGGCCACCAGGAATTTGCGACCCCTGAC	820
Db	69	TGCCAGGATAATTTCTGCTTGGCCATGGGCATCTGGCCACCAGGAATTTGCGACCCCTGAC	10
Qy	821	GATTACTCT	829
Db	9	GATTACTCT	1

Search completed: September 11, 2005, 10:36:34
Job time : 589.596 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 09:29:36 ; Search time 182.746 Seconds
(without alignments)
8479.259 Million cell updates/sec

Title: US-09-655-109A-4

Perfect score: 947

Sequence: 1 accanaccccaaaagaga.....tggcctcgagagatctatga 947

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgm2_6/ptodata/1/ina/5A COMB.seq:*
- 2: /cgm2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgm2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgm2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgm2_6/ptodata/1/ina/PTCUT COMB.seq:*
- 6: /cgm2_6/ptodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	93.4	9.9	376	US-09-513-999C-3095	Sequence 3095, Ap
2	57.6	6.1	7218	US-08-232-463-14	Sequence 14, Appl
3	54.8	5.8	1039	US-09-269-617-11	Sequence 11, Appl
4	53	5.6	1206	US-08-318-947A-1	Sequence 1, Appl
5	53	5.6	1206	US-08-795-303-1	Sequence 1, Appl
6	52	5.5	1025	US-09-269-617-13	Sequence 13, Appl
7	47.2	5.0	466	US-09-902-540-1318	Sequence 2061, Ap
8	43.6	4.6	614	US-09-902-540-1318	Sequence 1318, Ap
9	42	4.4	260	US-08-520-678A-29	Sequence 29, Appl
10	42	4.4	260	US-08-897-126-29	Sequence 29, Appl
11	41.8	4.4	612	US-09-902-540-1357	Sequence 1357, Ap
12	41.2	4.4	891	US-09-248-796A-11247	Sequence 11247, A
13	40.6	4.3	704	US-08-463-115-29	Sequence 29, Appl
14	40.6	4.3	704	US-08-465-388-29	Sequence 29, Appl
15	40.6	4.3	894	US-08-467-963C-28	Sequence 28, Appl
16	40.6	4.3	894	US-08-838-189D-28	Sequence 28, Appl
17	40.6	4.3	894	US-08-852-344D-28	Sequence 28, Appl
18	40.6	4.3	894	US-08-344-639E-28	Sequence 28, Appl
19	40.6	4.3	920	US-08-467-963C-7	Sequence 7, Appl
20	40.6	4.3	920	US-08-838-189D-7	Sequence 7, Appl
21	40.6	4.3	920	US-08-852-344D-7	Sequence 7, Appl
22	40.6	4.3	920	US-08-344-639E-7	Sequence 7, Appl
23	40.6	4.3	920	US-08-467-969A-7	Sequence 7, Appl
24	40.6	4.3	920	US-08-467-961A-7	Sequence 7, Appl
25	40.6	4.3	920	US-08-001-554A-7	Sequence 7, Appl
26	40.6	4.3	2223	US-08-257-073-4	Sequence 4, Appl
27	40.4	4.3	254964	US-09-949-016-12583	Sequence 12583, A

ALIGNMENTS

RESULT 1

US-09-513-999C-3095
Sequence 3095, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59 US2 REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 3095

LENGTH: 376

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 69..374

FEATURE:

NAME/KEY: misc_feature

LOCATION: 367

OTHER INFORMATION: m=a or c

FEATURE:

NAME/KEY: UNSURE

LOCATION: 100

OTHER INFORMATION: Xaa=Lys or Thr

US-09-513-999C-3095

Query Match 9.9% Score 93.4; DB 4; Length 376;

Best Local Similarity 61.7%; Pred. No. 3.4e-19;

Matches 148; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy	27	ATTCGGATCTTCGAGGCCGGAAGCGCGACCTTCGGAACGCGCGAGGCTTCAAGTGCATGATGT	86
Db	133	ACTGGGACTGTAGGCTCTGCACCTTCGGAACGCGCGAGGCTTCAAGTGCATGATGT	192
Qy	87	GCAGTGTGAGAAAGGCACCTCCACGAAACCTCGATCAATTTCTCAGCTGTGGCNC	146
Db	193	GCAGTGTGCGAAGGGCACCTCCACCGGAAACCTCGATCAATTTCTCAGCTGTGGCNC	252
Qy	147	AACAAGTGGCACACAGTATGCCACCCCTTAAAGGAGAGAGAGAGAGAG	206
Db	253	AGCAGGTTCATCAGCAGTTGTGCTCTCACAGTCAAGAGAGAGAGAGATTAAG	312

Sequence 17392, A
Sequence 25, Appl
Sequence 13427, A
Sequence 11, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 24, Appl
Sequence 8, Appl
Sequence 2801, Ap
Sequence 13042, A
Sequence 8976, Ap
Sequence 12096, A
Sequence 14114, A
Sequence 16027, A
Sequence 19, Appl

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QY 207 TTGAAAAGCAGCAAAAGAGAACCTGAGAAGACAGGAAATTTAGTCTAGTGTACCA 266
Db 313 TAGAAAAAGAAAAAGTGAAGAAAGGAAACAACTAGCAAAAAAGAAATAGCCATAAGAMAACCA 372

RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F18
US-08-232-463-14

Query Match 6.1%; Score 57.6; DB 1; Length 7218;
Best Local Similarity 1.6%; Pred. No. 6e-07;
Matches 6; Conservative 227; Mismatches 142; Indels 0; Gaps 0;

QY 9 CAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCGCAACAGTCTGAAG 68
Db 1435 CRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1376

QY 69 CCTTTAAATCAGCATCTGGATGTGAGGAAGCAGCTCCACAGAAAACTTCGGATCA 128
Db 1375 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1316

QY 129 ATTCTAGCTGGTGCNCACAACTGGCACAACAGTATGCCACCCACCCCTAAAA 188
Db 1315 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1256

QY 189 AGGAGAAGAGGAGAAAGTTCAAAGCAGCAAGCAAGAAACCTCGAAGAAACAAGAA 248
Db 1255 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1196
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QY 249 TTAGTCTCTAGTGTACCAAGAAAAATACCAACAGAAACCAAACTGACATTC 308
Db 1195 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1136

QY 309 TGAAGATCTCTCTAGTGAAGCAACAGCATACAGTCTCAAAATGCTACACAAAGACCA 368
Db 1135 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1076

QY 369 GCGAAACAAATACCA 383
Db 1075 RRRRRRRRATCGCA 1061

RESULT 3
US-09-269-617-11
; Sequence 11, Application US/09269617
; Patent No. 6204253
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FACTORS THAT INTERACT WITH ONCOPROTEINS
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/269,617
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1039 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: B-lymphocyte
; IMMEDIATE SOURCE: Human cDNA library
; CLONE: SZ29
US-09-269-617-11

Query Match 5.8%; Score 54.8; DB 3; Length 1039;
Best Local Similarity 88.1%; Pred. No. 1.3e-06;
Matches 59; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACCAACCACCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCGCAACAG 60
Db 53 ACCAACCACCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCGCAATC 112

QY 61 TGCTGAA 67
Db 113 TGAAGCA 119

RESULT 4
US-08-318-947A-1
; Sequence 1, Application US/08318947A
; Patent No. 5798245
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
```

```
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,947A
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,530
; FILING DATE: 07-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A6462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEX: 6491103
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 172..648
;
; US-08-318-947A-1
;
; Query Match 5.6%; Score 53; DB 1; Length 1206;
; Best Local Similarity 98.1%; Pred. No. 5.4e-06;
; Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 ACCAATCCCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 54
; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 3 ACCAATCCCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 56
;
; RESULT 5
; US-08-795-303-1
; Sequence 1, Application US/08795303
; Patent No. 5948656
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,303
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/318,947
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; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: 08/133,530
; FILING DATE: 07-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A6462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEX: 6491103
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 172..648
;
; US-08-795-303-1
;
; Query Match 5.6%; Score 53; DB 2; Length 1206;
; Best Local Similarity 98.1%; Pred. No. 5.4e-06;
; Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; Qy 1 ACCAATCCCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 54
; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 3 ACCAATCCCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 56
;
; RESULT 6
; US-09-269-617-13
; Sequence 13, Application US/09269617
; Patent No. 6204253
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FACTORS THAT INTERACT WITH ONCOPROTEINS
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/269,617
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1025 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: B-lymphocyte
; IMMEDIATE SOURCE:
; LIBRARY: Human cDNA library
; CLONE: SZ33
;
; US-09-269-617-13
;
; Query Match 5.5%; Score 52; DB 3; Length 1025;
; Best Local Similarity 96.3%; Pred. No. 1e-05;
; Matches 52; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; Qy 1 ACCAATCCCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 54
; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 66 ACCAATCCCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 119
```

```
RESULT 7
US-09-621-976-2061
; Sequence 2061, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2061
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 65..265
; NAME/KEY: misc_feature
; LOCATION: 32
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-2061

Query Match      5.0%; Score 47.2; DB 4; Length 466;
Best Local Similarity 69.6%; Pred. No. 0.0002;
Matches 64; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 27 ATTGGATCTCGAGGCCGGAAGCGGACAGTGTGAAGCCTTTAATGCGAGTCT 86
Db 129 ACTGGAGCTGTAGCGTCTGCACTTCGGAACACGCGCGGCTTCAAGTGCATGAT 188
Qy 87 GCGATGTGAGGAAAGGACCTCCACCAGAAA 118
Db 189 GCGATGTGCGGAGGCGACCTCCACCAGAA 220

RESULT 8
US-09-902-540-1318
; Sequence 1318, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1318
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(614)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1318

Query Match      4.6%; Score 43.6; DB 4; Length 614;
Best Local Similarity 51.5%; Pred. No. 0.0034;
Matches 100; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 185 AAAAAGGAGAGAGGAGAAAGTTGAAAAGCAGGACAAAGAAACCTCGAAGACAAG 244
Db 419 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG 478
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Qy 245 GAAATTAGTCTCTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCAAGTCTGAC 304
Db 479 AAAAAAAAAAAAAACAACAAAAAATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 538
Qy 305 ATTCTGAAGATCCTCTCTAGTGAAGCAAAACAGCATACAGTCTCCTCAATGCTACAAACAAG 364
Db 539 ACAAGAAGAAAGACAAAAAAGAAAAAGAAACAAAAAAGAAATCAAAAAAGAA 598
Qy 365 ACCAGCGAACAAA 378
Db 599 AAAAAAGACAAAAA 612

RESULT 9
US-08-520-678A-29/c
; Sequence 29, Application US/08520678A
; Patent No. 5874565
; GENERAL INFORMATION:
; APPLICANT: Rice, Charles M.
; APPLICANT: Kolykhalov, Alexander A.
; TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
; TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,678A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henderson, Melodie W.
; REGISTRATION NUMBER: 37,848
; REFERENCE/DOCKET NUMBER: 6029-6836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-520-678A-29

Query Match      4.4%; Score 42; DB 2; Length 260;
Best Local Similarity 55.5%; Pred. No. 0.0062;
Matches 81; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Qy 239 GACAAGGAATTAGTCTCTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCAAG 298
Db 174 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 115
Qy 299 TCTGACATTCTGAAGATCCTCTCTAG 324
Db 114 AAAGAAATGGAGTGTATTATCTCTACCAG 89
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RESULT 13

US-08-463-115-29/c
; Sequence 29, Application US/08463115
; Patent No. 5703221
; GENERAL INFORMATION:
; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: AND RELATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,115
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: Four
; APPLICATION NUMBER: 08/157,811
; FILING DATE: No. 5703221ember 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION:
US-08-463-115-29

Query Match 4.3%; Score 40.6; DB 1; Length 704;
Best Local Similarity 48.1%; Pred. No. 0.033;
Matches 64; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
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DB 477 ANTNNAGGANGANGGNGGANNANNNGGNCNNGAGNANCTGGGGCAANAAGAG 418
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QY 309 TGAAGATCTCTCC 321
DB 357 TNNCNAATCCNCC 345

RESULT 14

US-08-465-388-29/c
; Sequence 29, Application US/08465388
; Patent No. 5753488
; GENERAL INFORMATION:
; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: AND RELATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,388
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: Four
; APPLICATION NUMBER: 08/157,811
; FILING DATE: No. 5753488ember 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION:
US-08-465-388-29

Query Match 4.3%; Score 40.6; DB 1; Length 704;
Best Local Similarity 48.1%; Pred. No. 0.033;
Matches 64; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 189 AGGAGAGAGGAGGAGAAAGTTGAAAGCAGGACAGAGAAACCTGAGAGAGACAGGAAA 248
DB 477 ANTNNAGGANGANGGNGGANNANNNGGNCNNGAGNANCTGGGGCAANAAGAG 418
QY 249 TTAGTCCTAGTGTACCAAGAAAAATACCAACAGAAAAACCAACCAAAAGTCTGACATTC 308
DB 417 TTNAGGNATNTGGTTGNAGAAACNTCCATNAANAANAANAANAAGGTTGTTGTG 358
QY 309 TGAAGATCTCTCC 321
DB 357 TNNCNAATCCNCC 345

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OM nucleic - nucleic search, using sw model

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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	870	91.9	1128	21	US-10-489-740-35
2	868.4	91.7	1036	21	US-10-505-680-569
3	868.4	91.7	1036	21	US-10-956-157-1792
4	868.4	91.7	1036	21	US-10-956-157-7027
5	859	90.7	2156	14	US-10-103-313-121
6	469.6	49.6	502	10	US-09-918-995-24859
7	428.6	45.3	429	9	US-09-864-761-4575

Sequence 35, Appl
Sequence 569, App
Sequence 1792, Ap
Sequence 7027, Ap
Sequence 121, App
Sequence 24859, A
Sequence 4575, Ap

8	357.4	37.7	719	9	US-09-764-848-12	Sequence 12, Appl
9	357.4	37.7	719	14	US-10-116-016-12	Sequence 24, Appl
10	357.4	37.7	719	14	US-10-103-313-247	Sequence 12, Appl
11	357.4	37.7	719	16	US-10-222-020-12	Sequence 570, App
12	317.8	33.6	400	21	US-10-505-680-570	Sequence 21320, A
13	232.4	24.5	253	9	US-09-864-761-21320	Sequence 10941, A
14	230.4	24.3	326	17	US-10-242-535A-10941	Sequence 10941, A
15	230.4	24.3	326	18	US-10-085-783A-10941	Sequence 571, App
16	197.8	20.9	467	21	US-10-505-680-571	Sequence 10204, A
17	167.4	17.7	470	9	US-09-864-761-10204	Sequence 54267, A
18	109.2	11.5	430	20	US-10-357-930-54267	Sequence 22728, A
19	97.6	10.3	466	10	US-09-918-995-22728	Sequence 4587, Ap
20	95.2	10.1	799	21	US-10-956-157-4587	Sequence 582, App
21	95.2	10.1	1033	9	US-09-954-531-582	Sequence 1649, Ap
22	95.2	10.1	1033	21	US-10-843-641A-1649	Sequence 35185, A
23	93.2	9.8	454	10	US-09-918-995-35185	Sequence 9822, Ap
24	89.6	9.5	600	21	US-10-956-157-9822	Sequence 20856, A
25	86.4	9.1	475	10	US-09-918-995-20856	Sequence 26844, A
26	75	7.9	75	9	US-09-864-761-26844	Sequence 12263, A
27	68.8	7.3	551	16	US-10-029-386-12263	Sequence 25964, A
28	61.2	6.5	186	16	US-10-029-386-25964	Sequence 29954, A
29	60.2	6.4	65	10	US-09-908-975-29954	Sequence 26081, A
30	57.8	6.1	969	20	US-10-363-345A-26081	Sequence 26082, A
31	57.8	6.1	969	21	US-10-363-345A-26082	Sequence 26081, A
32	57.8	6.1	969	21	US-10-363-483A-26081	Sequence 26082, A
33	57.8	6.1	969	21	US-10-363-483A-26082	Sequence 1, Appl
34	52	5.5	2098	18	US-10-296-987-1	Sequence 28883, A
35	51.6	5.4	535	20	US-10-363-345A-28883	Sequence 28884, A
36	51.6	5.4	535	20	US-10-363-345A-28884	Sequence 28883, A
37	51.6	5.4	535	21	US-10-363-483A-28884	Sequence 28884, A
38	51.6	5.4	535	21	US-10-363-483A-28884	Sequence 9297, Ap
39	51.4	5.4	788	20	US-10-363-345A-9297	Sequence 9298, Ap
40	51.4	5.4	788	21	US-10-363-345A-9297	Sequence 9297, Ap
41	51.4	5.4	788	21	US-10-363-483A-9297	Sequence 80472, A
42	51.4	5.4	788	21	US-10-363-483A-9297	Sequence 120013, A
43	48.6	5.1	350	20	US-10-425-115-80472	Sequence 182979, A
44	48.6	5.1	1062	20	US-10-425-115-120013	
45	48	5.1	574	20	US-10-425-115-182979	

ALIGNMENTS

RESULT 1

US-10-489-740-35
; Sequence 35, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: p9
; FILE REFERENCE: Angiogenesis PCT
; CURRENT APPLICATION NUMBER: US/10/489, 740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-740-35

Query Match 91.9%; Score 870; DB 21; Length 1128;
Best Local Similarity 98.0%; Pred. No. 2.8e-241;
Matches 879; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

Qy	24	GGAAATCGGATCTCGAGGCCACGAAGCCGAAACAGTCTGAAGCCTTTAAATGCAGCA	83
Db	219	GGTTTTGGGATCTGAGCGTCTGCACCTTCAGAAACAGTCTGAAGCCTTTAAATGCAGCA	278
Qy	84	TCGCGGATGTGAGGAGGACCTCCACACGAGAAACCTCGGATCAATTTCTCAGCTGGTGG	143
Db	279	TCGCGGATGTGAGGAGGACCTCCACACGAGAAACCTCGGATCAATTTCTCAGCTGGTGG	338

; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
 ; FILE REFERENCE: 031896-043000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US/10/956,157
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 319805
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1792
 ; LENGTH: 1036
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-956-157-1792

	Query Match	91.7%	Score 868.4	DB 21	Length 1036
	Best Local Similarity	97.9%	Pred. No. 7.8e-241		
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QY	24	GGAATTCGGATCTCTCGAGGCCACGAAAGCCGGAACAGTGTGTAAGCCCTTTAAATGCAGCA	83		
DB	135	GGTTTTGGGATTTAGTCGTCTGACCTTTCAGAAACAGTGTGTAAGCCCTTTAAATGCAGCA	194		
QY	84	TCTGCGATGTGAGGAAGGCCACCTCCACGAGAAACCTTCGATCAATTTCTCAGCTGGTGG	143		
DB	195	TCTGCGATGTGAGGAAGGCCACCTCCACGAGAAACCTTCGATCAATTTCTCAGCTGGTGG	254		
QY	144	CNCAACAAGTGCACACAGATATGTCACCCACACCCCTTAAAGAGGAGGAAGGAGA	203		
DB	255	CACAACAAGTGCACACAGATATGTCACCCACACCCCTTAAAGAGGAGGAAGGAGA	314		
QY	204	AAGTTGAAAGCAGGACCAAGAAACCTTGAGAAAGACAAGGAAATTAGTCTTAGTGTTA	263		
DB	315	AAGTTGAAAGCAGGACCAAGAAACCTTGAGAAAGACAAGGAAATTAGTCTTAGTGTTA	374		
QY	264	CCAAGAAATACCAACAGAAACCAACCAAGTCTGACATCTTGAAGATCCTCCTA	323		
DB	375	CCAAGAAATACCAACAGAAACCAACCAAGTCTGACATCTTGAAGATCCTCCTA	434		
QY	324	GTGAGCAACAGCATACAGTCTGCAATGCTTACAAACAAAGACGAGCAACCAATCACA	383		
DB	435	GTGAGCAACAGCATACAGTCTGCAATGCTTACAAACAAAGACGAGCAACCAATCACA	494		
QY	384	CCTCAAGGCCCGGCTGAAACACGTGGACAGGACATGTCACAGCAGTTGGCAGTAACTG	443		
DB	495	CCTCAAGGCCCGGCTGAAACACGTGGACAGGACATGTCACAGCAGTTGGCAGTAACTG	554		
QY	444	TGGGCAACGTACCGTCAATATTCACAGATTTAAGGAAAGATCGCTCTCATCGACAT	503		
DB	555	TGGGCAACGTACCGTCAATATTCACAGATTTAAGGAAAGATCGCTCTCATCGACAT	614		
QY	504	CCTCATCCACGTGACCTCCAGTGCAGGCTCAGAACAGCAGAACCCAGCAGCTCGGGT	563		
DB	615	CCTCATCCACGTGACCTCCAGTGCAGGCTCAGAACAGCAGAACCCAGCAGCTCGGGT	674		
QY	564	CAGAGAGCACAGCAAGGCTCTCCCGTTCCTCCACGCAAGAGGCGACATGTGAGCAG	623		
DB	675	CAGAGAGCACAGCAAGGCTCTCCCGTTCCTCCACGCAAGAGGCGACATGTGAGCAG	734		
QY	624	TCAATGATGAATCTTTCTGAAATGTCACATGGAATTTGTGAAACCTATGATCAGGGTATG	683		
DB	735	TCAATGATGAATCTTTCTGAAATGTCACATGGAATTTGTGAAACCTATGATCAGGGTATG	794		
QY	684	AAATTCAAACCTCCACCTGCCATCTGCTGCAATCCCTGGAGATCTTCTGTGACAT	743		
DB	795	AAATTCAAACCTCCACCTGCCATCTGCTGCAATCCCTGGAGATCTTCTGTGACAT	854		
QY	744	CGACCTCTTAGTGATGCTGCGAGGATAATTTCTGTGCTTGGCAGTGGGCACTCTGTCGACAT	803		
DB	855	CGACCTCTTAGTGATGCTGCGAGGATAATTTCTGTGCTTGGCAGTGGGCACTCTGTCGACAT	914		
QY	804	GAAATTCGCAACCCCTGACGATTAATCTTGACACTTTTATGATATCCATCTGTTTATATGAT	863		

Db	915	GAATTTCCGACCCCTGACGATTACTCTTGACACITTTTATGTATTCCATTTGTTTATATGAT	974
Qy	864	TTTCTTAACAATCATTTTATTAATTTGGATGCTCTCGAATCTACATTTTATAAAAAA	920
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RESULT 4			
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; Sequence 7027, Application US/10956157			
; Publication No. US20050118625A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William			
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH			
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES			
; FILE REFERENCE: 031896-043000 (AM 101081)			
; CURRENT APPLICATION NUMBER: US/10/956.157			
; CURRENT FILING DATE: 2004-10-04			
; NUMBER OF SEQ ID NOS: 319805			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 7027			
; LENGTH: 1036			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-956-157-7027			
Query Match 91.7%; Score 868.4; DB 21; Length 1036;			
Best Local Similarity 97.9%; Pred. No. 7.8e-241;			
Matches 878; Conservative 1; Mismatches 18; Indels 0; Gaps 0;			
Qy	24	GGAAATTCGGATCTTCGAGGCCACGAAGCCGAAACAGTGTCTGAAGCCCTTTAAATGCACGA	83
Db	135	GGTTTTCGGATTTGAGCGTCTGCAACCTTTCAGAAAACAGTGTCTGAAGCCCTTTAAATGCACGA	194
Qy	84	TCTCGGATGTCAGGAAGAGGCACTCCACACGAAAAACCTTCGGATCAATTTCTCAGCTGGTGG	143
Db	195	TCTCGGATGTCAGGAAGAGGCACTCCACACGAAAAACCTTCGGATCAATTTCTCAGCTGGTGG	254
Qy	144	CNCAACAAAGTGGCACAACAGATATGCAACCCCAACCCCAACCCCTTAAAAAGGAGAAAGGAGA	203
Db	255	CACAACAAAGTGGCACAACAGATATGCAACCCCAACCCCAACCCCTTAAAAAGGAGAAAGGAGA	314
Qy	204	AAGTTGAAAAGCAGGACAAAAGAGAAACCTCTGAGAAAGACAAGGAAATTTAGTCTCTAGTGTTA	263
Db	315	AAGTTGAAAAGCAGGACAAAAGAGAAACCTCTGAGAAAGACAAGGAAATTTAGTCTCTAGTGTTA	374
Qy	264	CCAGAAAAATACCAACACGAGAAAAACCAACCAAGTCTGACATTTCTGAAAAGATCCTCCTTA	323
Db	375	CCAGAAAAATACCAACACGAGAAAAACCAACCAAGTCTGACATTTCTGAAAAGATCCTCCTTA	434
Qy	324	GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTTACAAACAAAGACGACGAAACAAATCACA	383
Db	435	GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTTACAAACAAAGACGACGAAACAAATCACA	494
Qy	384	CCTCAAGGCCCGGCTGAAAAACGTGGAACAGGACATCTGCAACAGAGTTGGCAGTTAACTG	443
Db	495	CCTCAAGGCCCGGCTGAAAAACGTGGAACAGGACATCTGCAACAGAGTTGGCAGTTAACTG	554
Qy	444	TGGGCAACGTACCCGTATTATACAGACTTTTAAGGAAAAGACTCGCTCCTCATCGACAT	503
Db	555	TGGGCAACGTACCCGTATTATACAGACTTTTAAGGAAAAGACTCGCTCCTCATCGACAT	614
Qy	504	CCTCATCCACAGTGCACCTCCAGTGCAGGCTCAGAAACAGCAGAAACAGASCAGCTCGGGGT	563
Db	615	CCTCATCCACAGTGCACCTCCAGTGCAGGCTCAGAAACAGCAGAAACAGASCAGCTCGGGGT	674
Qy	564	CAGAGAGCACAGCAAGGGCTCCTCCCGTTCTTCCACGCAAAAGGGCGACATGTGACGAC	623
Db	675	CAGAGAGCACAGCAAGGGCTCCTCCCGTTCTTCCACGCAAAAGGGCGACATGTGACGAC	734
Qy	624	TCAATGATGAATCTTTTCTGAAATTCACATGGAATTTGTAATTTGTAATTTGAGGTATG	683

Db 735 TCATGATGATCTTCTGAAATGACATGGAAATGTGAAACTATGAAATCAGGGTATG 794
Qy 684 AATTTAAAACCTCCACCTGCCCATGCTGTGATCCCTGGAGAAATCTTCTGTGGACAT 743
Db 795 AATTTAAAACCTCCACCTGCCCATGCTGTGATCCCTGGAGAAATCTTCTGTGGACAT 854
Qy 744 CGACCTCTTAGTGTGCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAG 803
Db 855 CGACCTCTTAGTGTGCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAG 914
Qy 804 GAATTTGCGACCTCGACGATTAATCTTGACACTTTTATGATGATTTTATGAT 863
Db 915 GAATTTGCGACCTCGACGATTAATCTTGACACTTTTATGATGATTTTATGAT 974
Qy 864 TTTCTTAACAATCATTTATTAATGGATGCTCTCTGAATCTACTTTTTATAAAAAA 920
Db 975 TTTCTTAACAATCATTTATTAATGGATGCTCTCTGAATCTACTTTTTATAAAAAA 1031

RESULT 5

US-10-103-313-121
; Sequence 121, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FUZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-121

Query Match 90.7%; Score 859; DB 14; Length 2156;
Best Local Similarity 97.9%; Pred. No. 6.4e-238;
Matches 879; Conservative 1; Mismatches 17; Indels 1; Gaps 1;

Qy 24 GGAATTCGGATCTCGAGGCCACGAGGCCGGAACAGTGTGAGCCCTTTAAATGACGA 83
Db 64 GGTTTGGGATTGTAGCGTCTGCACCTTCAGAAACAGTGTGAGCCCTTTAAATGACGA 123
Qy 84 TCTGCGATGTGAGAAAGGCACCTCCACCA-GAAACCTCGGATCAATCTCAGCTGGTG 142
Db 124 TCTGCGATGTGAGAAAGGCACCTCCACCATGAAACCTCGGATCAATCTCAGCTGGTG 183
Qy 143 GCNCAACAGTGGCACAACAGTATGCCACCCACCCCTAAAAAGGAGAAAGAGGAG 202
Db 184 GCACAACAGTGGCACAACAGTATGCCACCCACCCCTAAAAAGGAGAAAGAGGAG 243
Qy 203 AAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAATAGTCTAGTGT 252
Db 244 AAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAATAGTCTAGTGT 303
Qy 263 ACCAAGAAAATACCAACAGAAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCT 322
Db 304 ACCAAGAAAATACCAACAGAAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCT 353
Qy 323 AGTGAAGCAACAGCATACAGTCTGCAATGTCTACAAAGACCCAGCGAAACAAATCAC 382
Db 364 AGTGAAGCAACAGCATACAGTCTGCAATGTCTACAAAGACCCAGCGAAACAAATCAC 423
Qy 383 ACCTCAAGGCCCGGCTGAAAACGTGGACAGGACCTGCCACAGTGGCAGTAAC 442
Db 424 ACCTCAAGGCCCGGCTGAAAACGTGGACAGGACCTGCCACAGTGGCAGTAAC 483
Qy 443 GTGGGCAACGTCAACCGTCAATTAACAGACTTTTAAGGAAAGACTCGCTCTCATCGACA 502

Db 484 GTGGGCAACGTCAACCGTCAATTAACAGACTTTTAAGGAAAGACTCGCTCTCATCGACA 543
Qy 503 TCCTCATCCACAGTGAACCTCCAGTGCAGGGTCAGAAACAGACAGAACCCAGAGCAGCTCGGG 562
Db 544 TCCTCATCCACAGTGAACCTCCAGTGCAGGGTCAGAAACAGACAGAACCCAGAGCAGCTCGGG 603
Qy 563 TCAGAGAGCACAGACAAGGGCTCTCCCGTCTCTCCACGCCAAAGGGCGACATGTGACGA 622
Db 604 TCAGAGAGCACAGACAAGGGCTCTCCCGTCTCTCCACGCCAAAGGGCGACATGTGACGA 663
Qy 623 GTCAATGATGAATCTTTCTGAAATTCACATGGAATTTGTGAAACTATGAATCAGGGTAT 682
Db 664 GTCAATGATGAATCTTTCTGAAATTCACATGGAATTTGTGAAACTATGAATCAGGGTAT 723
Qy 683 GAAATTTAAAACCTCCACCTGCCCATGCTGCTTGCATTCCTGGAGAAATCTTCTGTGGACA 742
Db 724 GAAATTTAAAACCTCCACCTGCCCATGCTGCTTGCATTCCTGGAGAAATCTTCTGTGGACA 783
Qy 743 TCGACCTCTTAGTGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAA 802
Db 784 TCGACCTCTTAGTGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAA 843
Qy 803 GGAATTTGCGACCTCGACGATTAATCTTGACACTTTTATGATTTCCATTTGTTTATATGA 862
Db 844 GGAATTTGCGACCTCGACGATTAATCTTGACACTTTTATGATTTCCATTTGTTTATATGA 903
Qy 863 TTTTCTTAACAATCATTTATTAATGGATGCTGCTCTGAATCTACTTTTTATAAAAAA 920
Db 904 TTTTCTTAACAATCATTTATTAATGGATGCTGCTCTGAATCTACTTTTTATAAAAAA 961

RESULT 6

US-09-918-995-24859
; Sequence 24859, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24859
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(502)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24859

Query Match 49.6%; Score 469.6; DB 10; Length 502;
Best Local Similarity 96.6%; Pred. No. 2.6e-125;
Matches 478; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 337 CATACAGTCTGCAATGCTTACAAAGACCCAGCGAAACAAATCACACCTCAAGGCCCG 396
Db 8 CNAATAGATCGCTATAGCGCTTCGAGGACCCAGCGAAACAAATCACACCTCAAGGCCCG 67
Qy 397 GCTGAAAAACGTGGACAGGACCTGCAAGCAGTTGGCAGTAACCTGTGGCAACCGTCAC 456
Db 68 GCTGAAAAACGTGGACAGGACCTGCAAGCAGTTGGCAGTAACCTGTGGCAACCGTCAC 127
Qy 457 CGTCATTAATACAGACTTTTAAGAAAAAGACTCGCTCTCATGACATCTCATCCACAGT 516
Db 128 CGTCATTAATACAGACTTTTAAGAAAAAGACTCGCTCTCATGACATCTCATCCACAGT 187
Qy 517 GACCTCCAGTGCAGGGTCAGAAACAGACAGAACCCAGAGCAGCTCGGGGTGAGAGACAGA 576

Db 188 GACCTCAGTGCAGGGTTCAGAACAGCAGAACAGCAGCTCGGGTTCAGAGACAGCAGA 247
Qy 577 CAAGGGTCTCTCCGTTCTCCAGCCAAAGGGGAGCATGTCAGCAGTCAATCATGAATC 636
Db 248 CAAGGGTCTCTCCGTTCTCCAGCCAAAGGGGAGCATGTCAGCAGTCAATCATGAATC 307
Qy 637 TTCTGAAATTCACATGGAATTTGAAACTATGAATCAGGGTATGAAATTCAAAACCT 696
Db 308 TTCTGAAATTCACATGGAATTTGAAACTATGAATCAGGGTATGAAATTCAAAACCT 367
Qy 697 CCACCTGCCATGCTGCTGCATCCCTGGAGAAATCTTCTGTGAGACATCGACCTTTAGTG 756
Db 368 CCACCTGCCATGCTGCTGCATCCCTGGAGAAATCTTCTGTGAGACATCGACCTTTAGTG 427
Qy 757 ATGCTGCCAGATTAATTTCTGCTTGCATGGGATCTGGCCACCAAGGAATTTTCGACCC 816
Db 428 ATGCTGCCAGATTAATTTCTGCTTGCATGGGATCTGGCCACCAAGGAATTTTCGACCC 487
Qy 817 TGACGATTACTCTTG 831
Db 488 TGACGATTACTCTTG 502

RESULT 7
US-09-864-761-4575/c
; Sequence 4575, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4575
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; INFORMATION: MAP TO AC012553.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
US-09-864-761-4575
Query Match 45.3%; Score 428.6; DB 9; Length 429;
Best Local Similarity 99.8%; Pred. No. 1.9e-113;
Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 401 AAAAACTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACCTGTGGCAACGTCACCGTC 460
Db 429 AAAAACTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACCTGTGGCAACGTCACCGTC 370
Qy 461 ATTATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACATCCATCCACAGTGACC 520
Db 369 ATTATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACATCCATCCACAGTGACC 310
Qy 521 TCCAGTGCAGGGTCAGAAACAGCAGAACAGCAGCTCGGGGTTCAGAGACAGACAGCAAG 580
Db 309 TCCAGTGCAGGGTCAGAAACAGCAGAACAGCAGCTCGGGGTTCAGAGACAGACAGCAAG 250
Qy 581 GGCTCTCTCCGTTCTCCAGCCAAAGGGGAGCATGTCAGCAGTCAATGATGATCTTTC 640
Db 249 GGCTCTCTCCGTTCTCCAGCCAAAGGGGAGCATGTCAGCAGTCAATGATGATCTTTC 190
Qy 641 TGAATTCACATGGAATTTGTAAGAACTATGATCAGGGTATGAAATTCAAAACCTCCAC 700
Db 189 TGAATTCACATGGAATTTGTAAGAACTATGATCAGGGTATGAAATTCAAAACCTCCAC 130
Qy 701 CTGCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGTGATGC 760
Db 129 CTGCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGTGATGC 70
Qy 761 TGCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAAGGAATTTTCGACCTTGAC 820
Db 69 TGCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAAGGAATTTTCGACCTTGAC 10
Qy 821 GATTACTCT 829
Db 9 GATTACTCT 1
RESULT 8
US-09-764-848-12
; Sequence 12, Application US/09764848
; Patent No. US2002007270A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ08
; CURRENT APPLICATION NUMBER: US/09/764,848
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 719

us-09-655-109a-4.rnpb

1	PRIOR APPLICATION NUMBER: 60/218,299
2	PRIOR FILING DATE: 2000-07-14
3	PRIOR APPLICATION NUMBER: 60/225,757
4	PRIOR FILING DATE: 2000-08-14
5	PRIOR APPLICATION NUMBER: 60/226,868
6	PRIOR FILING DATE: 2000-08-22
7	PRIOR APPLICATION NUMBER: 60/216,647
8	PRIOR FILING DATE: 2000-07-07
9	PRIOR APPLICATION NUMBER: 60/225,267

; PRIOR APPLICATION NUMBER: 60/216,880
 ;
 ; PRIOR FILING DATE: 2000-07-07
 ;
 ; PRIOR APPLICATION NUMBER: 60/225,270
 ;

PRIOR APPLICATION NUMBER: 60/251,861	PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834	PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/234,274	PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234,223	PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/228,924	PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/224,518	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,369	PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/224,519	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,964	PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241,809	PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249,299	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/236,327	PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/241,785	PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617	

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, PRIOR FILING DATE: 2000-08-14
, PRIOR APPLICATION NUMBER: 60/236,368
, PRIOR FILING DATE: 2000-09-29
, PRIOR APPLICATION NUMBER: 60/251,856
, PRIOR FILING DATE: 2000-12-08
, PRIOR APPLICATION NUMBER: 60/251,868
, PRIOR FILING DATE: 2000-12-08
, PRIOR APPLICATION NUMBER: 60/229,344
, PRIOR FILING DATE: 2000-09-01
, PRIOR APPLICATION NUMBER: 60/234,997
, PRIOR FILING DATE: 2000-09-25
, PRIOR APPLICATION NUMBER: 60/229,343
, PRIOR FILING DATE: 2000-09-01
, PRIOR APPLICATION NUMBER: 60/229,345
, PRIOR FILING DATE: 2000-09-01
, PRIOR APPLICATION NUMBER: 60/229,287
, PRIOR FILING DATE: 2000-09-01
, PRIOR APPLICATION NUMBER: 60/229,513
, PRIOR FILING DATE: 2000-09-05
, PRIOR APPLICATION NUMBER: 60/231,413
, PRIOR FILING DATE: 2000-09-08
, PRIOR APPLICATION NUMBER: 60/229,509
, PRIOR FILING DATE: 2000-09-05
, PRIOR APPLICATION NUMBER: 60/236,367
, PRIOR FILING DATE: 2000-09-29
, PRIOR APPLICATION NUMBER: 60/237,039
, PRIOR FILING DATE: 2000-10-02
, PRIOR APPLICATION NUMBER: 60/237,038
, PRIOR FILING DATE: 2000-10-02
, PRIOR APPLICATION NUMBER: 60/236,370

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200

; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08

Query Match 37.7%; Score 357.4; DB 16; Length 719;
Best Local Similarity 94.4%; Pred. No. 1.2e-92;
Matches 389; Conservative 2; Mismatches 19; Indels 2; Gaps 2;

QY	24	GGNATTGGGATCTCGAGGCGCCAGAGGCGGAAACAGTCTGAAGCCTTTAAATGACGA	83
DB	53	GGTTTGGGATTTAGCGCTTGACCTTCAGAAACAGTGTGAAGCCTTTAAATGACGA	112
QY	84	TCGCGATGTGAGGAAAGGCACCTCCACCAGAAACCTCGGATCAATTTCTCAGCTGGTG	143
DB	113	TCGCGATGTGAGGAAAGGCACCTCCACCAGAAACCTCGGATCAATTTCTCAGCTGGTG	172
QY	144	CNCAACAAGTGGCACAACAGTATGTCACCCACCACCCCTTAAAAAGGAGAGAGAGA	203
DB	173	CACAACAAGTGGCACAACAGTATGTCACCCACCACCCCTTAAAAAGGAGAGAGAGA	232
QY	204	AGTTCAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAATTTAGTCTTAGTGTTA	263
DB	233	AGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAATTTAGTCTTAGTGTTA	292
QY	264	CCAAGAAAATACCAACAAGAAAACCAAAACCAAGTCTGACATTTCTGAAGATCCTCCTA	323
DB	293	CCAAGAAAATACCAACAAGAAAACCAAAACCAAGTCTGACATTTCTGAAGATCCTCCTA	351
QY	324	GTGAAGCAAAACAGCATACAGTCTGCAATGCTTACAAAGACCGGAGAAACAAATCACA	383
DB	352	GTGAAGCAAAACAGCATACAGTCTGCAATGCTTACAAAGACCGGAGAAACAAATCACA	411
QY	384	CCTCAAGGCCCCGGCTGAAAACGT-GGACAGGACACTGCACAGCAGTTGG	434
DB	412	CCTCAAGGCCCCGGCTGAAAACGTGGGACAGGACACTGCACAGCAGTTGG	463

RESULT 12

US-10-505-680-570/c
; Sequence 570, Application US/10505680
; Publication No. US2005009592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.
; APPLICANT: Boyd, Jeff
; APPLICANT: Liu, Edison T.
; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TAI
; FILE REFERENCE: 4239-64452
; CURRENT APPLICATION NUMBER: US/10/505,680

CURRENT FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/357,031
PRIOR FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 822
SOFTWARE: PatentIn version 3.1
SEQ ID NO 570
LENGTH: 400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(400)
OTHER INFORMATION: "n" represents an unknown nucleotide
US-10-505-680-570

Query Match 33.6%; Score 317.8; DB 21; Length 400;
Best Local Similarity 93.5%; Pred. No. 2.5e-81;
Matches 375; Conservative 1; Mismatches 15; Indels 10; Gaps 4;
Qy 522 CCAGTGCAGGTC-AGAACAGCAGAACCCAGASCAGCTCGGGGTGAGAGAG-----CACAG 575
Db 400 CCAGTGCAGGTCAGAACAGCAGAACGACGACGCTCGGGGTGAGAGAGCAGCGGAC 341
Qy 576 ACAAGGGCTCTCCGCTTCCT---CCACGCCAAAGGGCGACATGTCAGCGATCAATGATG 632
Db 340 AAAGGGCTCTCCGCTTCCTTCNCAACCCCAAGGGCGACATGTCAGCGATCAATGATG 281
Qy 633 AATCTTTCTGAAATGACATGGAATTTGTGAACACTATGATCAGGGTATGAAATTCAAA 692
Db 280 AATCTTTCTGAAATGACATGGAATTTGTGAACACTATGATCAGGGTATGAAATTCAAA 221
Qy 693 ACCTCCACCTGCCATGCTGCTGCATCCCTGGAGATCTTCTGACATCGACCTCTT 752
Db 220 ACCTCCACCTGCCATGCTGCTGCATCCCTGGAGATCTTCTGACATCGACCTCTT 161
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Qy 813 ACCCTGAGGATCTCTTGACACTTTTATGATGATTCATGTTTATGATTTTCTTAAAC 872
Db 101 ACCCTGAGGATCTCTTGACACTTTTATGATGATTCATGTTTATGATTTTCTTAAAC 42
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RESULT 13
US-09-864-761-21320/C
Sequence 21320, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/006666

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 21320
LENGTH: 253
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC012553.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: NT HIT: g11431695, EVALUE 1.00e-127
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US-09-864-761-21320

Query Match 24.5%; Score 232.4; DB 9; Length 253;
Best Local Similarity 98.7%; Pred. No. 1.2e-56;
Matches 233; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 56 CAGAGACACAGACAGAGGGCTCTCCCGTTCCTCCAGCCCAAGGGGCGACATGTCA 1
RESULT 14
US-10-242-535A-10941
Sequence 10941, Application US/10242535A
Publication No. US20040013663A1

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; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
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; ORGANISM: Human
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; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
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Best Local Similarity 93.4%; Pred. No. 5.1e-56;
Matches 240; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy 264 CCAAGAAAATATACCAAC 280
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; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085.783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
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; OTHER INFORMATION: n is a, c, g, or t
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Best Local Similarity 93.4%; Pred. No. 5.1e-56;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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13	930.4	82.3	943	6	C0715417 Sequence
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15	881.4	77.9	947	6	AX114151 Sequence
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ALIGNMENTS

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LOCUS AX114152 1131 bp DNA linear
DEFINITION Sequence 5 from Patent EP1108785.
ACCESSION AX114152
VERSION AX114152.1 GI:14031160

KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Apoptin-associating protein
TITLE Patent: EP 1108785-A 5 20-JUN-2001;
JOURNAL Leadd B.V. (NL)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 5.1e-291;
Matches 1131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
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LOCUS AX092139 1131 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 9 from Patent W00116165.
ACCESSION AX092139
VERSION AX092139.1 GI:13444366
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Noteborn, M.H. and danen-van Oorschot, A.A.
Apoptin-associating protein
Patent: WO 0116165-A 9 08-MAR-2001;
Leadd B.V. (NL)
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Location/Qualifiers
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RESULT 3
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LOCUS AX138319 1131 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 9 from Patent EP1083224.
ACCESSION AX138319
VERSION AX138319.1 GI:14274285
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Noteborn,M.H. and danen-van Oorschot,A.A.
AUTHORS Apoptin-associating protein
TITLE Apoptin-associating protein
JOURNAL Patent: EP 1083224-A 9 14-MAR-2001;
Leadd B.V. (NL)
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Query Match 99.9%; Score 1129.4; DB 6; Length 1131;
Best Local Similarity 99.9%; Pred. No. 1.4e-290;
Matches 1130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCAACCAAAAGAGATCTGGAAT 60
Db 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCAACCAAAAGAGATCTGGAAT 60
61 TCGGATCTCGAGGCCACGAAGGCTTCTCTCGAGCGCGCGGTTTCGGCTTGGGG 120
61 TCGGATCTCGAGGCCACGAAGGCTTCTCTCGAGCGCGCGGTTTCGGCTTGGGG 120
121 GGGCGGGGTACAGCCCATCCATCCATGCGGCACAGAGAGCCCGCAGGCCCAAAA 180
121 GGGCGGGGTACAGCCCATCCATGACCATGGGCACAGAGAGCCCGCAGGCCCAAAA 180
181 AGACAAGCGAACTCTGCCGACAGCAAGAGGTTTTGGGATTTAGCGTCTGCACCTTCAGA 240
181 AGACAAGCGAACTCTGCCGACAGCAAGAGGTTTTGGGATTTAGCGTCTGCACCTTCAGA 240
241 AACAGTGTGAAGCCTTTTAAATGACGATCTGCGGATGTGAGAAAGGCACCTCCACCAGA 300
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Db AAACCTCGGATCAATTTCTCAGCTGCTGGGCAAAAGTGGGCAAAAGTATGCCACCCCA 360
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361 CCACCCCTTAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
421 AAAGCAAGAGAAATTAGTCTCTAGTGTTCACCAAGAGAAATATACCAAGAGAAATACCA 480
421 AAAGCAAGAGAAATTAGTCTCTAGTGTTCACCAAGAGAAATATACCAAGAGAAATACCA 480
481 AAGTCTGAATTTCTGAAGATCTCTTAGTGAGGAAACAGCATATACAGTCTGCAATGCT 540
481 AAGTCTGAATTTCTGAAGATCTCTTAGTGAGGAAACAGCATATACAGTCTGCAATGCT 540
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541 ACAACAAAGACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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661 AAGGAAAGACGCTGCTCTCATCGACATCTCTCATTCACAGTGACCTCCAGTGAGGGTCA 720
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721 GAACAGCAGAACGAGCAGCTCGGGTTCAGAGAGCAGACAGAGAGAGAGAGAGAGAGAG 780
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901 GCATCCCTGGAGAACTCTTCTGTGGACATCGACCTCTTAGTGATGCTGCGCAGGATAATTC 960
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961 TGCTTGCCATGGGCATCTGCCCAAGGAATTCGACCTCGACCTGACGATTACTCTTGACAC 1020
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1021 TTTTATGATTCATCTGTTTATATGATTTTCTTAACAATCATTTATATGATGCT 1080
1021 TTTTATGATTCATCTGTTTATATGATTTTCTTAACAATCATTTATATGATGCT 1080
1081 CCTGAATCTACTTTTATATAAAGGCCCTTCGTGGCCTCGAGAGATCTATGA 1131
1081 CCTGAATCTACTTTTATATAAAGGCCCTTCGTGGCCTCGAGAGATCTATGA 1131

RESULT 4
AX138332
LOCUS AX138332 1131 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 12 from Patent EP1081226.
ACCESSION AX138332
VERSION AX138332.1 GI:14274288
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Apoptin-associating protein
AUTHORS Apoptin-associating protein
TITLE Apoptin-associating protein
JOURNAL Patent: EP 1081226-A 12 07-MAR-2001;
Leadd B.V. (NL)
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FEATURES	Location/Qualifiers																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	</
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Db	841	AATTGTGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCATGCTGCTT	900		
Qy	901	GCATCCCTGGAGAACTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTC	960		
Db	901	GCATCCCTGGAGAACTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTC	960		
Qy	961	TGCTTGGCATGGGCATCTGGCCACCAAGAAATTCGACCCCTGACGATTACTCTTGACAC	1020		
Db	961	TGCTTGGCATGGGCATCTGGCCACCAAGAAATTCGACCCCTGACGATTACTCTTGACAC	1020		
Qy	1021	TTTTATGTATTCATTTGTTTTATATGATTTTCTTAAACAATCATTTATAATTGGATGTCT	1080		
Db	1021	TTTTATGTATTCATTTGTTTTATATGATTTTCTTAAACAATCATTTATAATTGGATGTCT	1080		
Qy	1081	CCTGAATCTACTTTTTATATAAAGGCTTCGTGGCTCGAGAGATCTATGA	1131		
Db	1081	CCTGAATCTACTTTTTATATAAAGGCTTCGTGGCTCGAGAGATCTATGA	1131		
RESULT 5	BD209971	3641 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	Human transcriptional regulator molecules.				
DEFINITION	BD209971				
ACCESSION	BD209971.1	GI:33019741			
VERSION	JP 2002513554-A/43.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 3641)				
AUTHORS	Hillman, J.L., Bandman, O., Lal, P., Yue, H., Reddy, R., Tang, T.Y., Gerstin, E.H., Patterson, C., Baughn, M.R., Azimzai, Y. and Lu, D.A.M.				
TITLE	Human transcriptional regulator molecules				
JOURNAL	Patent: JP 2002513554-A 43 14-MAY-2002;				
COMMENT	INCYTE PHARMACEUTICALS INC OS Homo sapiens (human) PN JP 2002513554-A/43 PD 14-MAY-2002 PF 04-MAY-1999 JP 2000547113 PR 05-MAY-1998 US 60/084254, 07-AUG-1998 US 60/095827 PR 02-OCT-1998 US 60/102745 PI JENNIFER L HILLMAN, OLGA BANDMAN, PREETI LAL, HENRY YUE, ROOPA PI REDDY, PI TOM Y TANG, EDWARD H GERSTIN, CHANDRA PATTERSON, MARIAH R BAUGHN, PI YALDA AZIMZAI, DYUNG AINA M LU PC C12N15/09, A61K39/00, A61K45/00, A61P35/00, A61P37/02, A61P43/00, PC C07K14/47, PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/68//C12P21/ PC 02, PC C12P21/08, C12N15/00, A61K37/02, C12N5/00 CC Incyte clone 3149729CB1 FH Key Location/Qualifiers FT source 1. .3641 FT /organism='Homo sapiens (human)'. FEATURES source 1. .3641 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'				
ORIGIN					
Query Match	90.3%; Score 1021; DB 6; Length 3641;				
Best Local Similarity	99.5%; Pred. No. 1.5e-261;				
Matches 1024; Conservative	0; Mismatches 5; Indels 0; Gaps 0;				
Qy	75	CCACGAAGCGCTTCTCTCCGAGCGCGCGCTTTTCGGCTTGGGGGGCGGGGTACAG	134		
Db	77	CCGACGCGCTTCTCTCCGAGCGCGCGCTTTTCGGCTTGGGGGGCGGGGTACAG	136		
Qy	135	CCCATCATGACCATGGCGCAACAGAGAGCCGACCGCCAAAAGACACAGCGAAACC	194		

Db 137 CCATCCATGACCATGGGCGACAAAGAGAGCCCGACAGCCGCAAAAAGACAGACGAAACC 196
Qy 195 TGCCGCGACGAGAGGTTTGGGATTTAGCGTCTGACCTTCAGAAACAGTCTGAAGC 254
Db 197 TGCCGCGACGAGAGGTTTGGGATTTAGCGTCTGACCTTCAGAAACAGTCTGAAGC 256
Qy 255 CTTTAAATGACGATCTCGCATGTGAGGAAAGGACCTCCACAGAGAAACCTCGGATCAA 314
Db 257 CTTTAAATGACGATCTCGCATGTGAGGAAAGGACCTCCACAGAGAAACCTCGGATCAA 316
Qy 315 TTCTCAGCTGGTGCAACAAGTGGGCAACAGTGGGCAACAGTATGCCACCCACCCCTTAAAA 374
Db 317 TTCTCAGCTGGTGCAACAAGTGGGCAACAGTATGCCACCCACCCCTTAAAA 376
Qy 375 GGAGAAAGAGGAGAAATTTGAAAGAGGAGGCAAGAGAAACCTGAGAAAGACAGAGGAAT 434
Db 377 GGAGAAAGAGGAGAAATTTGAAAGAGGAGGCAAGAGAAACCTGAGAAAGACAGAGGAAT 436
Qy 435 TAGTCTTAGTGTATACCAAGAAATATCAACAAGAAACCAAAACCAAGTCTGACATTTCT 494
Db 437 TAGTCTTAGTGTATACCAAGAAATATCAACAAGAAACCAAAACCAAGTCTGACATTTCT 496
Qy 495 GAAAGATCTCTTAGTGAAGCAACAGATACAGTCTGCAAAATGCTTACAAAGAACGAG 554
Db 497 GAAAGATCTCTTAGTGAAGCAACAGATACAGTCTGCAAAATGCTTACAAAGAACGAG 556
Qy 555 CGAAACAANTACACCTCAAGGCCCGGCTGAAAGAGCTGACAGAGGACCTGACAGCA 614
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Qy 615 GTTGGCAGTAACTGTGGCAAGCTCACCGTCAATATCACAGACTTTAAGGAAAGACTCG 674
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Qy 675 CTCCTCATCGACATCTCATCCACAGTGAACCTCAGTGCAGGGTCAGAAACAGACGAA 734
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Qy 735 GAGCAGCTCGGGGTGAGAGCAGACAGAGGGCTCTCCGTTCTCCAGCCGCAAGGG 794
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Qy 855 TGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCTGCTGATCCCTGGAGAA 914
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Qy 915 TCTTCTGAGACATCGACCTCTTAGTGAATGCTGCCAGGATTAATTTCTGCTTGGCATGGC 974
Db 917 TCTTCTGAGACATCGACCTCTTAGTGAATGCTGCCAGGATTAATTTCTGCTTGGCATGGC 976
Qy 975 ATCTGGCCACCAAGGAAATTCGACCCCTGACGATTAATTTCTGACATTTTATGATTTCCA 1034
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Qy 1035 TTGTTTTATATGATTTCTTAAACATCAATTAATTAATTTGATGATGCTGCTGATTTT 1094
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Qy 1095 TTATAAAAA 1103
Db 1097 TTATAAAAA 1105

RESULT 6
AX821956
LOCUS AX821956 1036 bp DNA linear PAT 10-DEC-2003
DEFINITION Sequence 84 from Patent WO03068961.
ACCESSION AX821956
VERSION AX821956.1 GI:39725177

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Andrews, P.A., Walsh, J.A. and Gokhale, P.A.
METHOD to modify differentiation of pluripotential stem cells
TITLE Patent: WO 03068961-A 84 21-AUG-2003;
JOURNAL Axordia Limited (GB)
FEATURES
Location/Qualifiers
source 1..1036
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 90.1%; Score 1019.4; DB 6; Length 1036;
Best Local Similarity 99.4%; Pred. No. 3.5e-261;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 75 CCACGAGGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTCGGGGGGCGGGGTACAG 134
Db 1 CCCGACGGGTTTCTCTCCGAGCGCGCGGTTTCGGCTTCGGGGGGCGGGGTACAG 60
Qy 135 CCCATCATGACCATGGGCGACAAAGAGAGCCCGACGACGCAAAAGACAAAGCAAGCAAAACC 194
Db 61 CCCATCATGACCATGGGCGACAAAGAGAGCCCGACGACGCAAAAGACAAAGCAAGCAAAACC 120
Qy 195 TGCCGAGAGAGGGTTTGGGATTTAGCGTCTGACCTTCAGAAACAGTCTGAAGC 254
Db 121 TGCCGAGAGAGGGTTTGGGATTTAGCGTCTGACCTTCAGAAACAGTCTGAAGC 180
Qy 255 CTTTAAATGACGATCTCGCATGTGAGGAAAGGACCTCCACAGAGAAACCTCGGATCAA 314
Db 181 CTTTAAATGACGATCTCGCATGTGAGGAAAGGACCTCCACAGAGAAACCTCGGATCAA 240
Qy 315 TTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGCCACCCACCCACCCCTTAAAA 374
Db 241 TTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGCCACCCACCCCTTAAAA 300
Qy 375 GGAGAAAGAGGAGAAATTTGAAAGAGGAGCAAAAGAGAAACCTGAGAAAGACAGGAAT 434
Db 301 GGAGAAAGAGGAGAAATTTGAAAGAGGAGCAAAAGAGAAACCTGAGAAAGACAGGAAT 360
Qy 435 TAGTCTTAGTGTATACCAAGAAATATCCAAAGAAACCAAAACCAAGTCTGACATTTCT 494
Db 361 TAGTCTTAGTGTATACCAAGAAATATCCAAAGAAACCAAAACCAAGTCTGACATTTCT 420
Qy 495 GAAAGATCTCTCTAGTGAAGCAACAGCATAACAGTCTGCAAAATGCTTACAAAGAACGAG 554
Db 421 GAAAGATCTCTCTAGTGAAGCAACAGCATAACAGTCTGCAAAATGCTTACAAAGAACGAG 480
Qy 555 CGAAACAATATCACCTCAAGGCCCGGCTGAAAGAGCTGAGAGGAGCTGACAGCA 614
Db 481 CGAAACAATATCACCTCAAGGCCCGGCTGAAAGAGCTGAGAGGAGCTGACAGCA 540
Qy 615 GTTGGCAGTAACTGTGGCAAGCTCACCGTCAATATCAAGACTTTAAGGAAAGACTCG 674
Db 541 GTTGGCAGTAACTGTGGCAAGCTCACCGTCAATATCAAGACTTTAAGGAAAGACTCG 600
Qy 675 CTCTCATCGACATCTCTCATCCAGTGAACCTCCAGTGCAGGGTCAGAAACAGCAAGCA 734
Db 601 CTCTCATCGACATCTCTCATCCAGTGAACCTCCAGTGCAGGGTCAGAAACAGCAAGCA 660
Qy 735 GAGCAGCTCGGGGTGAGAGGAGCAGAAAGGGCTCTCCGTTCTCCAGCCGCAAGGG 794
Db 661 GAGCAGCTCGGGGTGAGAGGAGCAGAAAGGGCTCTCCGTTCTCCAGCCGCAAGGG 720
Qy 795 CGACATGTCAGCAGTCAATGATGAATCTTTCTGAAATTCACATGGAATTTGTAATACTA 854
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Qy 915 TCTTCTGTGGACATCGACCTCTTAGTGTAGTGTGCGCAGGATAATTTCTGCTTGGCATGGGC 974
Db 841 TCTTCTGTGGACATCGACCTCTTAGTGTAGTGTGCGCAGGATATTTCTGCTTGGCATGGGC 900
Qy 975 ATCTGGCCACCAAGGAATTTGGCACCTGACGATTAATCTTGGACACTTTTATGATTTCCA 1034
Db 901 ATCTGGCCACCAAGGAATTTGGCACCTGACGATTAATCTTGGACACTTTTATGATTTCCA 960
Qy 1035 TTGTTTTATATGATTTTCTTAACAAATCATTTATATTTGGATGCTCTCGAATCTACTTT 1094
Db 961 TTGTTTTATATGATTTTCTTAACAAATCATTTATATTTGGATGCTCTCGAATCTACTTT 1020
Qy 1095 TTATAAAAA 1103
Db 1021 TAATAAAAA 1029

RESULT 7
AF179286 1036 bp mRNA linear PRI 21-AUG-2001
LOCUS Homo sapiens death effector domain-associated factor mRNA, complete cds.
ACCESSION AF179286
VERSION AF179286.1 GI:5802963
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1036)
AUTHORS Zheng L.X., Yoo T. and Lenardo, M.J.
TITLE A novel protein associated with Caspase-10 DED domain
JOURNAL Unpublished
MEDLINE 3 (bases 1 to 1036)
PUBMED Zheng L.X., Yoo T. and Lenardo, M.J.
REFERENCE 2 (bases 1 to 1036)
AUTHORS Zheng L.X., Yoo T. and Lenardo, M.J.
TITLE A novel protein associated with Caspase-10 DED domain
JOURNAL Unpublished
MEDLINE 3 (bases 1 to 1036)
PUBMED Zheng L.X., Yoo T. and Lenardo, M.J.
REFERENCE 3 (bases 1 to 1036)
AUTHORS Zheng L.X., Yoo T. and Lenardo, M.J.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1999) NIAID/LI, NIH, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES
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Db 1021 TAATAAAAA 1029
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RESULT 8	
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DEFINITION	Homo sapiens RING1 and YY1 binding protein, mRNA (cDNA clone
ACCESSION	MGC:23015 IMAGE:4902201), complete cds.
VERSION	BC014959.1 GI:15928992
KEYWORDS	MGC.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	1 (bases 1 to 1128)
	Strausberg,R.D., Feingold,B.A., Grouse,L.H., Derge,J.G.,
	Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
	Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
	Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
	Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
	Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
	Schettz,T.B., Brownstein,M.J., Udwin,T.B., Toshiyuki,S.,
	Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
	Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
	McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
	Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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	Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
	Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E.,
	Schneider,A., Schein,J.E., Jones,S.J. and Marra,M.A.
	Generation and initial analysis of more than 15,000 full-length
	human and mouse cDNA sequences
TITLE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL	12477932
PUBMED	2 (bases 1 to 1128)
REFERENCE	Strausberg,R.
AUTHORS	Direct Submission
TITLE	Submitted (01-OCT-2001) National Institutes of Health, Mammalian
JOURNAL	Gene Collection (MGC), Cancer Genomics Office, National Cancer
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
	USA.
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk
	Email: cgapbs-r@mail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Genome Sequence Centre,
	BC Cancer Agency, Vancouver, BC, Canada
	info@bcgsc.bc.ca
	Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
	Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
	Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
	Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
	Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,
	Farvaneh Seadi, JR Santos, Angelique Schnerch, Ursula Skalska,
	Duane Smalios, Jeff Scott, Miranda Tsai, George Yang, Jacque
	Schein, Asim Siddiqui, Rob Holt, Marco Marra.
	Clone distribution: MGC clone distribution information can be found
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RESULT 10
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LOCUS Homo sapiens YEAF1 mRNA for YF1 and E4TF1 associated factor 1,
DEFINITION complete cds.
ACCESSION AB029551
VERSION AB029551.1 GI:6714542
KEYWORDS YF1 and E4TF1 associated factor 1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Sawa, C., Yoshikawa, T., Matsuda-Suzuki, F., Delehouzee, S., Goto, M.,
Watanabe, H., Sawada, J., Kataoka, K. and Handa, H.
YEAF1/RYPB and YAF-2 are functionally distinct members of a
cofactor family for the YF1 and E4TF1/hGABP transcription factors
J. Biol. Chem. 277 (25), 22484-22490 (2002)
22063331
11953439
2 (bases 1 to 4700)
Sawa, C., Sawada, J. and Handa, H.
Direct Submission
Submitted (03-JUL-1999) Chika Sawa, Tokyo Institute of Technology,
BioScience and Biotechnology; 4259 Nagatsuta-cho Midori-ku,
Yokohama, Kanagawa 226-8503, Japan
(E-mail: Chika.Sawa@hms.harvard.edu,
URL: http://www.handa.bio.titech.ac.jp/,
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FEATURES
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VERSION AY228125.1 GI:29423710
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS
1 (bases 1 to 1021)
Danen-van Oorschot,A.A.M., Voiskamp,P., Seelen,M.C., van Milteneburg,M.H., Bolk,M.W., Tait,S.W., Boesen-de Cock,J.G., Rohn,J.L., Borst,J. and Noteborn,M.H.
Human death effector domain-associated factor interacts with the viral apoptosis agonist Apoptin and exerts tumor-preferential cell killing
Cell Death Differ. 11 (5), 564-573 (2004)
14765135
2 (bases 1 to 1021)
Danen-van Oorschot,A.A.M., Boesen-de Cock,J.G.R., Borst,J. and Noteborn,M.H.M.
AAP-1, a binding partner of Apoptin, induces cell death in human tumor cells but not in normal diploid cells
Unpublished
3 (bases 1 to 1021)
Danen-van Oorschot,A.A.M., Boesen-de Cock,J.G.R., Borst,J. and Noteborn,M.H.M.
Direct Submission
Submitted (31-JAN-2003) Leadd BV, Wassenaarseweg 72, Leiden 2333 AL, The Netherlands
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AX092138

LOCUS

DEFINITION Sequence 8 from Patent WO0116165.

ACCESSION AX092138

VERSION AX092138.1 GI:13444365

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Noteborn, M.H. and danen-van Oorschot, A.A.

JOURNAL Apoptin-associating protein

Leadd B.V. (NL) Patent: WO 0116165-A 8 08-MAR-2001;

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

1..947

/note="AAP-1-a nucleic acid wherein N can be A, C, G or T."

misc_feature

1..947

ORIGIN

Query Match 77.9%; Score 881.4; DB 6; Length 947;

Best Local Similarity 97.6%; Pred. No. 2.8e-224;

Matches 902; Conservative 2; Mismatches 19; Indels 1; Gaps 1;

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Db 84 TCTGCGATGTGAGAAAGGCACCTCCACAGAAACCTCGGATCAATTTCTCAGCTGGTGG 143

Qy 329 CACAACAGTGGCAACAGATATGCCACCCACCCCTTAAAAAGGAGAAAGAGAGA 388

Db 144 CNCAACAGTGGCAACAGATATGCCACCCACCCCTTAAAAAGGAGAAAGAGAGA 203

Qy 389 AGTTGAAAGCAGGACAAAGAAACCTGAGAAACAGAAAGAAATAGTCTTAGTGTGA 448

Db 204 AGTTGAAAGCAGGACAAAGAAACCTGAGAAACAGAAAGAAATAGTCTTAGTGTGA 263

Qy 449 CCAAGAAATATCCAAACAGAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 508

Db 264 CCAAGAAATATCCAAACAGAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 323

Qy 509 GTGAAGCAACAGCATACTGCAATATGCTCAACAAAGACCGAGCAACAAATCAACA 568

Db 324 GTGAAGCAACAGCATACTGCAATATGCTCAACAAAGACCGAGCAACAAATCAACA 383

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Db 384 CTTCAAGGCCCGGCTGAAACAGTGCAGAGGACCTGCACAGCAGTGGCAGTAACCTG 443

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RESULT 15			
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Matches			
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 8780412

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1129.4	99.9	1131	5	Aaf57185 Apoptin-a
4	1021	90.3	3641	3	Aa52452 HTRM Clon
5	1019.4	90.1	1036	10	Adk66994 Gene #84
6	1019.4	90.1	1036	10	Adk61399 Human c
7	1019.4	90.1	1128	8	AcF34480 Gene enco
8	1017.8	90.0	4700	10	AdD18793 Human dis
9	935.8	82.7	2156	4	Aa534877 Human enco
10	935.8	82.7	2156	10	AdC46035 Human neo
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12	881.4	77.9	947	5	Aaf55404 Nucleotid
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C	24	427.4	37.8	429	4	AAK30143	Aak30143 Human bon
C	25	427.4	37.8	429	4	AAK04634	Aak04634 Human bra
C	26	427.4	37.8	429	4	ABS29793	AbS29793 Human liv
C	27	427.4	37.8	429	5	AAI04546	Aai04546 Probe #45
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C	37	332.8	20.6	253	4	AAK43164	Aak43164 Human bon
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ALIGNMENTS

RESULT 1
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ID AAF55596 standard; cDNA; 1131 BP.

AC AAF55596;

DT 29-MAY-2001 (first entry)

DB Nucleotide sequence of apoptin-associating protein 1 cDNA clone b.

KW Apoptin-associating protein; AAP; apoptosis; cell proliferation;
cell death; autoimmune disease; cancer; ss.

OS Homo sapiens.

PN WO200116165-A2.

PD 08-MAR-2001.

PF 01-SEP-2000; 2000WO-NL000612.

PR 02-SEP-1999; 99EP-00202858.

PR 21-OCT-1999; 99EP-00203465.

XX (LEAD-) LEADD BV.

XX Noteborn MHM, Danen-Van Oorschot AAAM;

XX WPI; 2001-235090/24.

XX New nucleic acids encoding apoptin-associating proteins useful for
inducing apoptosis, particularly p53 independent apoptosis, or for
treating cancers or autoimmune diseases.

XX Claim 6; Fig 2; 50pp; English.

XX The present sequence encodes a human apoptin-associating protein 1
(AAP1). The protein is capable of providing apoptosis. AAP polypeptides
and polynucleotides are useful for inducing apoptosis, particularly when
apoptosis is p53-independent. They may be used to produce pharmaceutical
compositions which are used for treating a disease where enhanced cell
proliferation or decreased cell death is observed, particularly in cancer
or in autoimmune diseases, for diagnosing a disease related with

CC aberrancies in the apoptotic process, and for detecting the presence of
CC cancer cells or cells that are prone to cancer
XX
SQ Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
Query Match 99.9%; Score 1129.4; DB 4; Length 1131;
Best Local Similarity 99.9%; Pred. No. 3e-310;
Matches 1130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 481 AAGTCTGACATTTCTGAAGATCTCTCTAGTGAAGCAACAGCATACTGCAAAATGCT 540
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Qy 1081 CTGGAATCTACTTTTATATAAAGGCTTCGTGGCCTCGAGAGATCTATGA 1131
Db 1081 CCTGAATCTACTTTTATATAAAGGCTTCGTGGCCTCGAGAGATCTATGA 1131
RESULT 2
AAF55405 standard; DNA; 1131 BP.
XX
AC AAF55405;
DT 29-MAY-2001 (first entry)
XX
Nucleotide sequence of an apoptin-associating protein.
DE
XX
XX Apoptin-associating proteinaceous substance; cell proliferation;
KW apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer;
KW autoimmune disease; 88.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1. .828
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FT CDS 829. .939
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EF1081226-A1.
PN
XX
PD 07-MAR-2001.
XX
PF 02-SEP-1999; 99EP-00202858.
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PR 02-SEP-1999; 99EP-00202858.
XX
(LEAD-) LEADD BV.
XX
WPI; 2001-219813/23.
DR P-PSDB; AAB67559, AAB67560, AAB67561, AAB67562, AAB67563.
XX
XX Novel isolated or recombinant apoptin-associating proteinaceous
PT substance, apoptin-associating protein 1, useful for inducing apoptosis
PT for treating cancer or autoimmune diseases caused by aberrant apoptosis.
PS Claim 4; Fig 2; 29pp; English.
XX
CC The present sequence encodes an apoptin-associating proteinaceous
CC substance (apoptin-associating protein 1 (AAP-1)), which is capable of
CC inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for
CC inducing a p53-independent apoptosis. They are used for treating a
CC disease where enhanced proliferation or decreased cell death is observed
CC e.g. cancer or autoimmune disease. They are also used for diagnosis of
CC diseases related with aberrations in the apoptotic process such as cancer
CC and autoimmune diseases

CC of the AAP-1-b cDNA clone encoding a partial AAP-1-b protein

Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
SQ
XX

Query Match 99.9% Score 1129.4 DB 5 Length 1131;

Best Local Similarity 99.9%; Pred. No. 3e-310;
Matches 1130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	1	TATAACTATCTTATTCGATGTAAGATACCCCAACCAACCCAAAAGAGATCTGGAA	60
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Qy	241	AAACAGTGTGAAGCCTTTAAATGACGATCTGCGATGTGAGAAAGCAGCCTCCACCCAGA	300
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Qy	961	TGCTTGGCATGGGCATCTGGGCCAACAGGAAATTTTCGACCCCTGACGATTACTTTTGACAC	1020

CC differences in gene sequences among normal, carrier and affected
CC individuals. Using diagnostic assays, cancer can be detected prior to the
CC appearance of clinical symptoms and thereby progression of cancer can be
CC prevented by aggressive treatment or preventive measures
XX
SQ

Sequence 3641 BP; 1081 A; 718 C; 738 G; 1104 T; 0 U; 0 Other;

Query Match 90.3%; Score 1021; DB 3; Length 3641;
Best Local Similarity 99.5%; Pred. No. 3.8e-279;
Matches 1024; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 75 CCACGAAGCGCTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGTACAG 134
DB 77 CCGGAGCGGCTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGTACAG 136
QY 135 CCATTCATGACATGCGGCGCAAGAGAGAGCCGACAGCCCAAAAGACAGCGAACC 194
DB 137 CCCATCCATGACATGCGGCGCAAGAGAGAGCCGACAGCCCAAAAGACAGCGAACC 196
QY 195 TGCCGCGAGCAAGGGTTTTCGGATTGTAGCGTCTGCACCTTTCAGAAACAGTCTGAAGC 254
DB 197 TGCCGCGAGCAAGGGTTTTCGGATTGTAGCGTCTGCACCTTTCAGAAACAGTCTGAAGC 256
QY 255 CTTTAAATGCAGCATCTCGCATGTGAGGAAAGGACCTTCCACCGAAACCTCGGATCAA 314
DB 257 CTTTAAATGCAGCATCTCGCATGTGAGGAAAGGACCTTCCACCGAAACCTCGGATCAA 316
QY 315 TTCTCAGCTGTGGCAAAAGTGGGCAACAGTATGCGACCCGACCCCTTAAAAA 374
DB 317 TTCTCAGCTGTGGCAAAAGTGGGCAACAGTATGCGACCCGACCCCTTAAAAA 376
QY 375 GGAGAGAGAGAGAAAGTTGAAAGAGCAGCAAGAGAGAACTCGAGAAAGCAAGGAAAT 434
DB 377 GGAGAGAGAGAGAAAGTTGAAAGAGCAGCAAGAGAGAACTCGAGAAAGCAAGGAAAT 436
QY 435 TAGTCCTAGTGTACCAAGAAAAATACCAACAGAAAAACCAAAAGTCTGACATTCT 494
DB 437 TAGTCCTAGTGTACCAAGAAAAATACCAACAGAAAAACCAAAAGTCTGACATTCT 496
QY 495 GAAAGATCCTCTAGTGAAGCAACAGCATACAGTCTGCAATGCTCAACAAAGACGAG 554
DB 497 GAAAGATCCTCTAGTGAAGCAACAGCATACAGTCTGCAATGCTCAACAAAGACGAG 556
QY 555 CGAAACAAATCACACCTCAAGCCCGCGCTGAAAACGTGACAGGACACTGCACAGCA 614
DB 557 CGAAACAAATCACACCTCAAGCCCGCGCTGAAAACGTGACAGGACACTGCACAGCA 616
QY 615 GTTGGCAGTAACTGTGGCAACGTCACCGTCAATTATCACAGACTTTAAGGAAAAAGCTCG 674
DB 617 GTTGGCAGTAACTGTGGCAACGTCACCGTCAATTATCACAGACTTTAAGGAAAAAGCTCG 676
QY 675 CTCCTCATCGACATCCTCATCCAGTGAACCTTCCAGTGGAGGTCAGAAACAGCAGAACCA 734
DB 677 CTCCTCATCGACATCCTCATCCAGTGAACCTTCCAGTGGAGGTCAGAAACAGCAGAACCA 736
QY 735 GAGCAGCTCGGGTTCAGAGAGCAGACAGAGGGCTCTCCGTTCTCCAGCCCAAGGG 794
DB 737 GAGCAGCTCGGGTTCAGAGAGCAGACAGAGGGCTCTCCGTTCTCCAGCCCAAGGG 796
QY 795 CGACATGTCCAGAGTCAATGATGAATCTTTGTGAAATTCGACATGGAATTTGTGAAACTA 854
DB 797 CGACATGTCCAGAGTCAATGATGAATCTTTGTGAAATTCGACATGGAATTTGTGAAACTA 856
QY 855 TGAATCAGGGTATGAAATTTCAAAACCTCCACTGCGCCATGCTGCTTGCATCCCTGGAGAA 914
DB 857 TGAATCAGGGTATGAAATTTCAAAACCTCCACTGCGCCATGCTGCTTGCATCCCTGGAGAA 916
QY 915 TCTTCTGTGGCATCGACCTCTAGTGTGATGCTGCCAGGATATTTCTGCTGCCATGGGC 974
DB 917 TCTTCTGTGGCATCGACCTCTAGTGTGATGCTGCCAGGATATTTCTGCTGCCATGGGC 976
QY 975 ATCTGCGCCACCAAGGAAATTTCCGACCCCTGACGATTAATCTTTCGACACTTTTATGATTCGA 1034

DB 977 ATCTGCCCAAGGAATTTCCGACCCCTGACGATTAATCTTTCGACACTTTTATGATTCGA 1036
QY 1035 TTGTTTTATATGATTTTCTTAACAATCATTTATAAATGGATGTGCTCCTGAATCTACTTT 1094
DB 1037 TTGTTTTATATGATTTTCTTAACAATCATTTATAAATGGATGTGCTCCTGAATCTACTTT 1096
QY 1095 TTATAAAAA 1103
DB 1097 TTATAAAAA 1105
RESULT 5
ID ADK66994 standard; DNA; 1036 BP.
XX
AC ADK66994;
XX
DT 06-MAY-2004 (first entry)
XX
DE Gene #84 for inhibitory RNA to manipulate stem cell phenotype.
XX
KW ds; gene; inhibitory RNA; RNAi; Notch signaling target gene; phenotype;
XX
KW pluripotent stem cell.
XX
OS Homo sapiens.
XX
PN WO2003068961-A2.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-GB000579.
XX
PR 13-FEB-2002; 2002GB-00003359.
XX
PR 13-FEB-2002; 2002GB-00003387.
XX
PA (AXOR-) AXORDIA LTD.
XX
PI Andrews P, Walsh J, Gokhale P;
XX
XX WPI; 2003-697528/66.
XX
PT New inhibitory RNA molecule having double stranded RNA molecules, useful
PT for manipulating the phenotype of stem cells, preferably pluripotent
PT stem cells.
XX
PS Disclosure; SEQ ID NO 84; 157pp; English.
XX
CC The invention relates to an inhibitory RNA (RNAi) molecule derived from a
CC nucleic acid molecule comprising a defined nucleic acid sequences given
CC in the specification or a sequence which hybridizes to the sequences and
CC encodes a Notch signaling target gene or which is a degenerate as a
CC result of the genetic code of the sequences. The methods and compositions
CC of the present invention are useful for manipulating the phenotype of
CC stem cells, preferably pluripotent stem cells. This sequence corresponds
CC to one of the nucleic acid molecules of the invention.
SQ Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;
Query Match 90.1%; Score 1019.4; DB 10; Length 1036;
Best Local Similarity 99.4%; Pred. No. 5.6e-279;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 75 CCACGAAGCGCTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGTACAG 134
DB 1 CCCGAGCGGCTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGTACAG 60
QY 135 CCCATCCATGACATGCGGCGCAAGAGAGAGCCGACAGCCCAAAAGACAGCGAACC 194
DB 61 CCCATCCATGACATGCGGCGCAAGAGAGAGCCGACAGCCCAAAAGACAGCGAACC 120
QY 195 TGCCGCGAGCAAGGGTTTTCGGATTGTAGCGTCTGCACCTTTCAGAAACAGTCTGAAGC 254
DB 121 TGCCGCGAGCAAGGGTTTTCGGATTGTAGCGTCTGCACCTTTCAGAAACAGTCTGAAGC 180

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QY 255 CTTTAAATGACGATCTCGATGTGAGGAAGGCACTCCACAGAAACCTCGATCAA 314
Db 181 CTTTAAATGACGATCTCGATGTGAGGAAGGCACTCCACAGAAACCTCGATCAA 240
QY 315 TTCTCAGCTGGTGGCAACAAGTGGCAACAGTATGCCACCCACACCCCTAAAAA 374
Db 241 TTCTCAGCTGGTGGCAACAAGTGGCAACAGTATGCCACCCACACCCCTAAAAA 300
QY 375 GGAGAAGAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAT 434
Db 301 GGAGAAGAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAT 360
QY 435 TAGTCTAGTGTATACCAAGAAAATACCAAGAAAACCAAAACCAAGTCTGATTTCT 494
Db 361 TAGTCTAGTGTATACCAAGAAAATACCAAGAAAACCAAAACCAAGTCTGATTTCT 420
QY 495 GAAAGATCCTCTAGTGAAGCAACAGCATACTGTGCAAAATGCTACAAACAAAGACCAG 554
Db 421 GAAAGATCCTCTAGTGAAGCAACAGCATACTGTGCAAAATGCTACAAACAAAGACCAG 480
QY 555 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACGTTGACAGAGCACTGCACAGCA 614
Db 481 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACGTTGACAGAGCACTGCACAGCA 540
QY 615 GTTGGCAGTAACTCTGGGCAACGTCACCGTCATTATCACAGACTTTTAAGGAAAGACTCG 674
Db 541 GTTGGCAGTAACTCTGGGCAACGTCACCGTCATTATCACAGACTTTTAAGGAAAGACTCG 600
QY 675 CTCCTCATCGACATCTCATCCACAGTGACCTCCAGTGCAGGGTTCAGAACAGCAGAACCA 734
Db 601 CTCCTCATCGACATCTCATCCACAGTGACCTCCAGTGCAGGGTTCAGAACAGCAGAACCA 660
QY 735 GAGCAGCTCGGGGTTCAGAGACACAGCAAGGGCTCTCCGGTTCCTCCAGCGCAAGGG 794
Db 661 GAGCAGCTCGGGGTTCAGAGACACAGCAAGGGCTCTCCGGTTCCTCCAGCGCAAGGG 720
QY 795 CGACATCTGACGACTCAATGATGATCTTTGTGAAATTCACATGGAAATTTGTGAAACTA 854
Db 721 CGACATCTGACGACTCAATGATGATCTTTGTGAAATTCACATGGAAATTTGTGAAACTA 780
QY 855 TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGTGCATCCCTCGAGAA 914
Db 781 TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGTGCATCCCTCGAGAA 840
QY 915 TCTTCTGTGACATCGACCTCTTAGTGATGTGCGCAGGATAATTTCTGTCTGCCATGGGC 974
Db 841 TCTTCTGTGACATCGACCTCTTAGTGATGTGCGCAGGATAATTTCTGTCTGCCATGGGC 900
QY 975 ATCTGGCCACCAAGGAATTTGCGACCCCTGACGATTACTCTTGACACTTTTATGTATCCA 1034
Db 901 ATCTGGCCACCAAGGAATTTGCGACCCCTGACGATTACTCTTTGACACTTTTATGTATCCA 960
QY 1035 TTGTTTTATATGATTTTCTTAACAATCATTTATAATTTGGATGTGCTCCTGAACTACTTT 1094
Db 961 TTGTTTTATATGATTTTCTTAACAATCATTTATAATTTGGATGTGCTCCTGAACTACTTT 1020
QY 1095 TTATAAAAA 1103
Db 1021 TAATAAAAA 1029
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RESULT 6

ADK61399
ID ADK61399 standard; DNA; 1036 BP.

XX AC ADK61399;

XX AC ADK61399;

DT 06-MAY-2004 (first entry)

XX Ovarian cancer-related DNA #554 with altered ovarian cancer expression.

XX ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;

gene expression; primer; cancer.

Homo sapiens.

WO2003068054-A2.

21-AUG-2003.

13-FEB-2003; 2003WO-US004688.

13-FEB-2002; 2002US-0357031P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

(SLOK) SLOAN KETTERING INST CANCER RES.

Jazaeri AA, Boyd J, Liu ET;

WPI; 2003-689589/65.

Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by determining a pattern of expression in the ovarian tumor of several markers.

Disclosure; SEQ ID NO 569; 137bp; English.

The invention relates to a method of classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a pattern of expression in the ovarian tumor of several markers given in the specification; and (2) comparing a similarity of the pattern of expression of the markers in the ovarian tumor to a pattern of expression of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-like or non-BRCA-like tumor. The method is useful for classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor. This sequence corresponds to an ovarian cancer -related gene having an altered pattern of expression in ovarian cancer. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences).

Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;

Query Match 90.1%; Score 1019.4; DB 10; Length 1036;

Best Local Similarity 99.4%; Pred. No. 5.6e-279;

Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 75 CCACGAAGGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 134

Db 1 CC CGGACGGGTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 60

QY 135 CCCATCCATGACCATCGGCGACAAAGAGAGCCGACGAGCCCAAAAAGACGAGAAACC 194

Db 61 CCATTCATGACCATCGGCGACAAAGAGAGCCGACGAGCCCAAAAAGACGAGAAACC 120

QY 195 TGCCGAGACGAGAGGGTTTTGGGATTTGTAGCGTCTGCACCTTCAGAAAACAGTCTGAAGC 254

Db 121 TGCCGAGACGAGAGGGTTTTGGGATTTGTAGCGTCTGCACCTTCAGAAAACAGTCTGAAGC 180

QY 255 CTTTAAATGACGATCTCGATGTGAGGAAGGCACTCCACAGAAAACCTCGGATCAA 314

Db 181 CTTTAAATGACGATCTCGATGTGAGGAAGGCACTCCACAGAAAACCTCGGATCAA 240

QY 315 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACACCCCTTAAAAA 374

Db 241 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACACCCCTTAAAAA 300

QY 375 GGAGAAGAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTTGAGAAAGACAAGGAAT 434

Db 301 GGAGAAGAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTTGAGAAAGACAAGGAAT 360

QY 435 TAGTCTAGTGTATACCAAGAAAATACCAAGAAAACCAAAACCAAGTCTGACATTCT 494

Db 361 TAGTCTAGTGTATACCAAGAAAATACCAAGAAAACCAAAACCAAGTCTGACATTCT 420

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QY 495 GAAAGATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAAGACCCAG 554
DB 421 GAAAGATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAAGACCCAG 480
QY 555 CGAAACAAATACACACCTCAAGGCCCGGCTGAAAAACGTGGACAGGAGCACTGGACAGCA 614
DB 481 CGAAACAAATACACACCTCAAGGCCCGGCTGAAAAACGTGGACAGGAGCACTGGACAGCA 540
QY 615 GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCATCAGACTTTTAAGGAAAGACTCG 674
DB 541 GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCATCAGACTTTTAAGGAAAGACTCG 600
QY 675 CTCCTCATCGACATCTCTCATCCACAGTACCTCCAGTGCAGGGTGCAGAACAGCAGAACCA 734
DB 601 CTCCTCATCGACATCTCTCATCCACAGTACCTCCAGTGCAGGGTGCAGAACAGCAGAACCA 660
QY 735 GAGCAGCTCGGGGTGAGAGGACAGACAGAGGGCTCTCCGTTCTCCAGCGCAAGGG 794
DB 661 GAGCAGCTCGGGGTGAGAGGACAGACAGAGGGCTCTCCGTTCTCCAGCGCAAGGG 720
QY 795 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTTGCACATGGAATTTGTGAAACTA 854
DB 721 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTTGCACATGGAATTTGTGAAACTA 780
QY 855 TGAATCAGGGTATCAAAATTCAAAACCTCCACCTGCCCATGCTGTGATCCCTCGAGAA 914
DB 781 TGAATCAGGGTATCAAAATTCAAAACCTCCACCTGCCCATGCTGTGATCCCTCGAGAA 840
QY 915 TCTTCTGTGGACATCGACCTCTTAGTGATGATGCTGCCAGGATAATTTCTGCTTGCATGGG 974
DB 841 TCTTCTGTGGACATCGACCTCTTAGTGATGATGCTGCCAGGATAATTTCTGCTTGCATGGG 900
QY 975 ATCTGGCCACCAAGGAATTTGGACCTCGAGTACTCTTGACACTTTTATGATTTCCA 1034
DB 901 ATCTGGCCACCAAGGAATTTGGACCTCGAGTACTCTTGACACTTTTATGATTTCCA 960
QY 1035 TTGTTTTATATGATTTCTCTAAACATATTATATTTGGAATGCTCTCTGAATCTACTTT 1094
DB 961 TTGTTTTATATGATTTCTCTAAACATATTATATTTGGAATGCTCTCTGAATCTACTTT 1020
QY 1095 TTATAAAAA 1103
DB 1021 TAATAAAAA 1029

RESULT 7
ACF34480
ID ACF34480 standard; DNA; 1128 BP.
XX AC ACF34480;
XX 15-OCT-2003 (first entry)
XX DE Gene encoding angiogenesis protein BNO98.
XX KW Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
XX KW antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;
XX KW gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;
XX KW diabetic retinopathy; cardiovascular disease; atherosclerosis;
XX KW ischemic limb disease; coronary artery disease; gene; ds.
XX OS Homo sapiens.
XX FN WO2003027285-A1.
XX PD 03-APR-2003.
XX PF 19-SEP-2002; 2002WO-AU001282.
XX PR 27-SEP-2001; 2001AU-00007973.
XX PR 27-SEP-2001; 2001AU-00007974.
XX PR 11-OCT-2001; 2001AU-00008210.
XX PR 29-OCT-2001; 2001AU-00008532.
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PR 13-NOV-2001; 2001AU-00008838.
PR 28-AUG-2002; 2002AU-00951032.
PA (BION-) BIONOMICS LTD.
XX Gamble JR, Hahn CN, Vadas MA;
PI WPI; 2003-354655/33.
XX P-PSDB; ABR64205.
DR New angiogenic genes and polypeptides, useful for diagnosing,
XX prognosticating or treating an angiogenesis-related disorder, e.g.
PT cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or
PT cardiovascular diseases.
XX Claim 2; SEQ ID NO 35; 90pp; English.
PS The invention relates to the isolation of novel genes (ACF34446-ACF34559)
XX encoding proteins (ABR64180-ABR64281) involved in the process of
CC angiogenesis. The nucleic acid molecules are useful in identifying and/or
CC obtaining full-length human genes involved in an angiogenic process. The
CC nucleic acid molecule, polypeptides or complexes encoded, cells or
CC genetically modified non-human animals derived from these are useful for
CC the screening of candidate pharmaceutical compounds used in treating
CC angiogenesis-related disorders. They are also useful for diagnosing,
CC prognosticating or treating an angiogenesis-related disorder, which
CC involves uncontrolled or enhanced angiogenesis or is a disorder in which
CC a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,
CC diabetic retinopathy, psoriasis or cardiovascular diseases such as
CC atherosclerosis), or involves inappropriately arrested or decreased
CC angiogenesis or is a disorder in which an expanding vasculature is of
CC benefit (e.g. ischemic limb disease or coronary artery disease). The
CC modulator of expression or activity of the polypeptide encoded by the
CC nucleic acid sequence is useful for manufacturing a medicament for the
CC treatment of an angiogenesis-related disorder. This sequence corresponds
CC to the gene encoding one of the novel angiogenic protein
XX SQ Sequence 1128 BP; 341 A; 290 C; 282 G; 215 T; 0 U; 0 Other;

Query Match 90.1%; Score 1019.4; DB 8; Length 1128;
Best Local Similarity 99.4%; Pred. No. 5.8e-279;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 75 CCACGAAGGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTCGGGGGGGGGGTACAG 134
DB 85 CCGGACGGGTTTCTCTCCGAGCGCGCGGTTTCGGCTTCGGGGGGGGGGTACAG 144
QY 135 CCATCATGATCCATGCGGCGACAAAGAGAGCCCGACGAGCCCAAAAGACAGCGAACC 194
DB 145 CCATCATGATCCATGCGGCGACAAAGAGAGCCCGACGAGCCCAAAAGACAGCGAACC 204
QY 195 TCGCGGACGAGGAGGTTTGGGATTTGCGCTTCGACCTTCAGAAACAGTCTGAAGC 254
DB 205 TCGCGGACGAGGAGGTTTGGGATTTGCGCTTCGACCTTCAGAAACAGTCTGAAGC 264
QY 255 CTTTAAATGACGATCTCGCATGTGAGGAAAGGACCTCCACGAGAAACCTCGGATCAA 314
DB 265 CTTTAAATGACGATCTCGCATGTGAGGAAAGGACCTCCACGAGAAACCTCGGATCAA 324
QY 315 TTCTAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACCACCCCTTAAAAA 374
DB 325 TTCTAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACCACCCCTTAAAAA 384
QY 375 GGAGAGAGGAGGAGGTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 434
DB 385 GGAGAGAGGAGGAGGTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 444
QY 435 TAGTCCTAGTGTACCAAGAAATATACCAAGAAATATACCAAGAAATATACCAAGTCTTCT 494
DB 445 TAGTCCTAGTGTACCAAGAAATATACCAAGAAATATACCAAGTCTTCTGACATTTCT 504
QY 495 GAAAGATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAAGACCCAG 554
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Db 505 GAAAGATCCTCTCTAGTAGAAGCAACACAGCATACAGTCTGCAAAATGCTACAAACAAAGACCAG 564
Qy 555 CGAAACAAATCACACCTCAGGCCCGCGCTGAAACAACTGGACAGAGCACTGCACAGCA 614
Db 565 CGAAACAAATCACACCTCAGGCCCGCGCTGAAACAACTGGACAGAGCACTGCACAGCA 624
Qy 615 GTTGGCAGTAACTGTGGCAACGTCACCGTCATTATCACAGACTTTAAAGGAAAGACTCG 674
Db 625 GTTGGCAGTAACTGTGGCAACGTCACCGTCATTATCACAGACTTTAAAGGAAAGACTCG 684
Qy 675 CTCCTCATCGACATCCTCATCCACAGTGACCTCCAGTGCAGGGGTGAGAACAGCAGACCA 734
Db 685 CTCCTCATCGACATCCTCATCCACAGTGACCTCCAGTGCAGGGGTGAGAACAGCAGACCA 744
Qy 735 GAGCAGCTCGGGGTGAGAGCAGACAGAGGGCTCCTCCGTTCTCCTCCAGCGCAAGGG 794
Db 745 GAGCAGCTCGGGGTGAGAGCAGACAGAGGGCTCCTCCGTTCTCCTCCAGCGCAAGGG 804
Qy 795 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTCACATGGAATTTGGAACACTA 854
Db 805 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTCACATGGAATTTGGAACACTA 864
Qy 855 TGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCTGTGCATCCCTCGAGAA 914
Db 865 TGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCTGTGCATCCCTCGAGAA 924
Qy 915 TCTTCTGTGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGC 974
Db 925 TCTTCTGTGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGC 984
Qy 975 ATCTGGCCACCAAGGAATTTGCAACCTGACGATTACTTTGACACATTTTATGATTCCA 1034
Db 985 ATCTGGCCACCAAGGAATTTGCAACCTGACGATTACTTTGACACATTTTATGATTCCA 1044
Qy 1035 TTGTTTTATGATTTTCTTAACATCAATTTATTAATTTGATGCTCTCGAATCTACTTT 1094
Db 1045 TTGTTTTATGATTTTCTTAACATCAATTTATTAATTTGATGCTCTCGAATCTACTTT 1104
Qy 1095 TTATAAAAA 1103
Db 1105 TTATAAAAA 1113

RESULT 8
ADD18793
ID ADD18793 standard; DNA; 4700 BP.

XX
AC
XX
DT 15-JAN-2004 (first entry)

XX
DE Human disease related protein DNA sequence SeqID224.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
XX antiarteriosclerotic; vulnery; gene therapy;
XX hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
XX inflammation; erythropoiesis; glycolysis; gluconeogenesis;
XX glucose transportation; catecholamine synthesis; iron transport;
XX nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
XX retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
XX inflammatory condition; wound healing; gene; ds.

OS Homo sapiens.

XX WO2003018621-A2.

XX
XX
PD 06-MAR-2003.

XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX

PA
XX
PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX
DR WPI; 2003-290046/28.
DR P-PSDB; ADD18792.
XX
PT New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
XX wound healing.
XX
PS Claim 27; SEQ ID NO 224; 424pp; English.
XX
CC This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnery activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX
SQ Sequence 4700 BP; 1411 A; 898 C; 942 G; 1446 T; 0 U; 3 Other;
Query Match 90.0%; Score 1017.8; DB 10; Length 4700;
Best Local Similarity 99.3%; Pred. No. 3.5e-278;
Matches 1022; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 75 CCACGAGGCGCTTTCTCTCCGAGCGCGCGCTTTTCGGCTTGGGGGGGGCGGGGTACAG 134
Db 126 CCGGACGCGGCTTTCTCTCCGAGCGCGCGCTTTTCGGCTTGGGGGGGGCGGGGTACAG 185
Qy 135 CCATCCATGACCATGGGGGACAGAGAGCCGACAGCCGCAAAAGACAGCGAAACC 194
Db 186 CCATCCATGACCATGGGGGACAGAGAGCCGACAGCCGCAAAAGACAGCGAAACC 245
Qy 195 TGCCGACAGAGAGGGTTTGGGATTTGAGCTGCTCAGCTTCAGAAAACAGTCTGAAGC 254
Db 246 TGCCGACAGAGAGGGTTTGGGATTTGAGCTGCTCAGCTTCAGAAAACAGTCTGAAGC 305
Qy 255 CTTTAAATGACGATCTGCGATGTGAGGAAAGGACCTCCACAGAAAACCTCGGATCAA 314
Db 306 CTTTAAATGACGATCTGCGATGTGAGGAAAGGACCTCCACAGAAAACCTCGGATCAA 365
Qy 315 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACCCACCCCTTAAAAA 374
Db 366 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACCCACCCCTTAAAAA 425
Qy 375 GGNAGAGAGGAGAAAGTTGAAAGCAGGACGAGAAAGAACCTGAGAAAGACAGAGAAAT 434
Db 426 GGNAGAGAGGAGAAAGTTGAAAGCAGGACGAGAAAGAACCTGAGAAAGACAGAGAAAT 485
Qy 435 TAGTCTCTAGTGTTCACCAAGAAAATACCAACAGAAAACCCAAACCAAAAGTCTGACATTC 494
Db 486 TAGTCTCTAGTGTTCACCAAGAAAATACCAACAGAAAACCCAAACCAAAAGTCTGACATTC 545
Qy 495 GAAAGATCTCTCTAGTGAAGCAACAGCATACGTCTGCAATGTCTACAAACAGACCAG 554
Db 546 GAAAGATCTCTCTAGTGAAGCAACAGCATACGTCTGCAATGTCTACAAACAGACCAG 605
Qy 555 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACACGTGGACAGGACACTGCACAGCA 614
Db 606 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACACGTGGACAGGACACTGCACAGCA 665
Qy 615 GTTGGCAGTAACTGTGGGCAACGTCAACCGTCAATTATCAGAGCTTTAAGGAAAAGACTCG 674

(OXFO-) OXFORD BIOMEDICA UK LTD.

Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

WPI; 2003-290046/28.

P-PSDB; ADD18792.

New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.

Claim 27; SEQ ID NO 224; 424pp; English.

This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, ophthalmological, antiarteriosclerotic or vulnery activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein encoding DNA sequence of the invention.

Sequence 4700 BP; 1411 A; 898 C; 942 G; 1446 T; 0 U; 3 Other;

```
Db 666 GTTGGCAGTAACTGTGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG 725
Qy 675 CTCCTCATCGACATCCTCATCCAGTCAGTCAGTCCAGTGCAGGGTCAGACAGCAGAACCA 734
Db 726 CTCCTCATCGACATCCTCATCCAGTCAGTCAGTCCAGTGCAGGGTCGGAACAGCAGAACCA 785
Qy 735 GAGCAGCTCGGGGTCTGAGAGCAGACAGACAGAGGGCTCCTCCCGTTCCTCCAGCCCAAGGG 794
Db 786 GAGCAGCTCGGGGTCTGAGAGCAGACAGACAGAGGGCTCCTCCCGTTCCTCCAGCCCAAGGG 845
Qy 795 CGACATGTCAGCAGTCATTAATGATGAATCTTTGTGAAATTCACATGGAATTTGTGAAACTA 854
Db 846 CGACATGTCAGCAGTCATTAATGATGAATCTTTGTGAAATTCACATGGAATTTGTGAAACTA 905
Qy 855 TGAATCAGGGTATGAATTCAAACCTCCACCTGCCATGCTGCTGCATCCCTGGAGAA 914
Db 906 TGAATCAGGGTATGAATTCAAACCTCCACCTGCCATGCTGCTGCATCCCTGGAGAA 965
Qy 915 TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGC 974
Db 966 TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGC 1025
Qy 975 ATCTGGCCACCAAGAAATTCGACCCCTGACGATTACTCTTGACACTTTTATGATTCCA 1034
Db 1026 ATCTGGCCACCAAGAAATTCGACCCCTGACGATTACTCTTGACACTTTTATGATTCCA 1085
Qy 1035 TTGTTTTATATGATTTCTTAACATCAATTTATATTTGATGCTGCTGATCTACTTTT 1094
Db 1086 TTGTTTTATATGATTTCTTAACATCAATTTATATTTGATGCTGCTGATCTACTTTT 1145
Qy 1095 TTATAAAAA 1103
Db 1146 TTATAAAAA 1154

RESULT 9
AAS34877
ID AAS34877 standard; cDNA; 2156 BP.
XX AC AAS34877;
XX DT 04-DEC-2001 (first entry)
XX DE cDNA encoding novel human neoplastic disease associated polypeptide #11.
KW Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
XX OS Homo sapiens.
XX WO200155163-A1.
XX PN 02-AUG-2001.
XX PD 17-JAN-2001; 2001WO-US001358.
XX PF 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 30-JUN-2000; 2000US-0215135P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
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PR	01-NOV-2000;	2000US-0244617P.	CC	disorders, pulmonary disorders, cardiovascular disorders and renal
PR	08-NOV-2000;	2000US-0246474P.	CC	disorders. The polynucleotide sequences of the invention are also useful
PR	08-NOV-2000;	2000US-0246475P.	CC	in gene therapy. AAS34767-AAS35050 represent cDNA sequences encoding for
PR	08-NOV-2000;	2000US-0246476P.	CC	the novel human neoplastic disease associated polypeptides of the
PR	08-NOV-2000;	2000US-0246477P.	CC	invention. Note: The sequence data for this patent did not form part of
PR	08-NOV-2000;	2000US-0246478P.	CC	the printed specification, but was obtained in electronic format directly
PR	08-NOV-2000;	2000US-0246523P.	CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
PR	08-NOV-2000;	2000US-0246524P.	XX	
PR	08-NOV-2000;	2000US-0246525P.	SQ	Sequence 2156 BP; 659 A; 465 C; 419 G; 613 T; 0 U; 0 Other;
PR	08-NOV-2000;	2000US-0246526P.		
PR	08-NOV-2000;	2000US-0246527P.		
PR	08-NOV-2000;	2000US-0246528P.		
PR	08-NOV-2000;	2000US-0246532P.		
PR	08-NOV-2000;	2000US-0246609P.		
PR	08-NOV-2000;	2000US-0246610P.		
PR	08-NOV-2000;	2000US-0246611P.		
PR	08-NOV-2000;	2000US-0246613P.		
PR	17-NOV-2000;	2000US-0249207P.		
PR	17-NOV-2000;	2000US-0249208P.		
PR	17-NOV-2000;	2000US-0249209P.		
PR	17-NOV-2000;	2000US-0249210P.		
PR	17-NOV-2000;	2000US-0249211P.		
PR	17-NOV-2000;	2000US-0249212P.		
PR	17-NOV-2000;	2000US-0249213P.		
PR	17-NOV-2000;	2000US-0249214P.		
PR	17-NOV-2000;	2000US-0249215P.		
PR	17-NOV-2000;	2000US-0249216P.		
PR	17-NOV-2000;	2000US-0249217P.		
PR	17-NOV-2000;	2000US-0249218P.		
PR	17-NOV-2000;	2000US-0249244P.		
PR	17-NOV-2000;	2000US-0249245P.		
PR	17-NOV-2000;	2000US-0249246P.		
PR	17-NOV-2000;	2000US-0249265P.		
PR	17-NOV-2000;	2000US-0249266P.		
PR	17-NOV-2000;	2000US-0249297P.		
PR	17-NOV-2000;	2000US-0249299P.		
PR	17-NOV-2000;	2000US-0249300P.		
PR	01-DEC-2000;	2000US-0250160P.		
PR	01-DEC-2000;	2000US-0250391P.		
PR	03-DEC-2000;	2000US-0251030P.		
PR	03-DEC-2000;	2000US-0251988P.		
PR	05-DEC-2000;	2000US-0256719P.		
PR	06-DEC-2000;	2000US-0251479P.		
PR	08-DEC-2000;	2000US-0251856P.		
PR	08-DEC-2000;	2000US-0251868P.		
PR	08-DEC-2000;	2000US-0251869P.		
PR	08-DEC-2000;	2000US-0251989P.		
PR	11-DEC-2000;	2000US-0254097P.		
PR	05-JAN-2001;	2001US-0259678P.		
XX	(HUMA-)	HUMAN GENOME SCI INC.		
PA	Rosen CA, Barash SC, Ruben SM;			
XX				
XX	WPI; 2001-465558/50.			
DR	P-PSDB; AAU21678.			
XX				
PT	Novel polypeptides and polynucleotides useful as diagnostic reagents to			
PT	diagnose diseases or disorders associated with aberrant expression or			
PT	activity of polypeptides, and for treating cancers, rheumatoid arthritis.			
XX				
PS	Claim 4; SEQ ID NO 121; 687pp; English.			
XX				
CC	The present invention relates to the isolation of novel human neoplastic			
CC	disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA			
CC	sequences encoding for these polypeptides. The sequences of the invention			
CC	are useful in the diagnosis, treatment, prevention and/or prognosis of			
CC	disorders involving neoplastic disease such as hyperproliferative			
CC	disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem			
CC	glioma, adult liver cancer, childhood cerebellar astrocytoma, or			
CC	Hodgkin's lymphoma). The sequences of the invention may also be useful			
CC	for treating other disorders such as neural disorders, immune system			
CC	disorders, muscular disorders, reproductive disorders, gastrointestinal			

CC	disorders, pulmonary disorders, cardiovascular disorders and renal
CC	disorders. The polynucleotide sequences of the invention are also useful
CC	in gene therapy. AAS34767-AAS35050 represent cDNA sequences encoding for
CC	the novel human neoplastic disease associated polypeptides of the
CC	invention. Note: The sequence data for this patent did not form part of
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 2156 BP; 659 A; 465 C; 419 G; 613 T; 0 U; 0 Other;
	Query Match 82.7%; Score 935.8; DB 4; Length 2156;
	Best Local Similarity 99.2%; Pred. No. 4.9e-255;
	Matches 951; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY	146 CCATGGCGACAAAGAGAGCCCGACAGGCCAAAAGACAAGGAAACCTGGCGAGAGC 205
DB	
	1 CCACGCGTCCGAAGAGAGCCCGACAGGCCAAAAGACAAGCGAACTCGCGAGAGC 60
QY	206 AAGGGTTTTGGGATTCTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGCA 265
DB	
	61 AAGGGTTTTGGGATTCTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGCA 120
QY	266 GCATCTGCGATGTGAGGAAAGGCACCTCCACCA-GAAAACTCGGATCAATTTCTCAGCTG 324
DB	
	121 GCATCTGCGATGTGAGGAAAGGCACCTCCACCATGAACCTCGGATCAATTTCTCAGCTG 180
QY	325 GTGGCAACAAGTGGCACAACAGTATGCCACCCCAACCCCTTAAAGAGAGAGAG 384
DB	
	181 GTGGCAACAAGTGGCACAACAGTATGCCACCCCAACCCCTTAAAGAGAGAGAG 240
QY	385 GAGAAAGTTGAAAAGCAGGACAAAGAGAACTCTGAGAAAGACAAGGAAATTTAGTCTTCTAGT 444
DB	
	241 GAGAAAGTTGAAAAGCAGGACAAAGAGAACTCTGAGAAAGACAAGGAAATTTAGTCTTCTAGT 300
QY	445 GTTACCAAGAAAATAACCAACAGAAAACCAACCAAGTCTGACATTTCTGAAAAGATCCT 504
DB	
	301 GTTACCAAGAAAATAACCAACAGAAAACCAACCAAGTCTGACATTTCTGAAAAGATCCT 360
QY	505 CTTAGTGAAGCAAAACAGCATACAGTCTGCAATGTCTACAAAGACCCAGCGAGCAAAAT 564
DB	
	361 CTTAGTGAAGCAAAACAGCATACAGTCTGCAATGTCTACAAAGACCCAGCGAGCAAAAT 420
QY	565 CACACCTCAAGCCCGCGCTGAAAACGTGGACAGGACACTGCACAGCAGTTGGCAGTA 624
DB	
	421 CACACCTCAAGCCCGCGCTGAAAACGTGGACAGGACACTGCACAGCAGTTGGCAGTA 480
QY	625 ACTGTGGGCAACGCTCACCCGTCATTATCACAGACTTTTAAGGAAAAGACTCGCTCCTCATCG 684
DB	
	481 ACTGTGGGCAACGCTCACCCGTCATTATCACAGACTTTTAAGGAAAAGACTCGCTCCTCATCG 540
QY	685 ACATCCTCATCCACAGTGAACCTCCAGTGCAGGGTCAAGAACAGGAGAACAGAGCAGCTCG 744
DB	
	541 ACATCCTCATCCACAGTGAACCTCCAGTGCAGGGTCAAGAACAGGAGAACAGAGCAGCTCG 600
QY	745 GGGTCAGAGAGCACAGACAGAGGGCTCTCCCGTTCTCCACGCCAAGGGCGACATGTCA 804
DB	
	601 GGGTCAGAGAGCACAGACAGAGGGCTCTCTCCCGTTCTCCACGCCAAGGGCGACATGTCA 660
QY	805 GCAGTCAATGATCAATCTTTTGTGAAATTCACATGGAATTTGAAACCTATGAATCAGGG 864
DB	
	661 GCAGTCAATGATCAATCTTTTGTGAAATTCACATGGAATTTGAAACCTATGAATCAGGG 720
QY	865 TATGAAATTCAAAACCTTCCACCTGCCATGCTGCTTGCATTCCTGTGAGAAATCTTCTGTGG 924
DB	
	721 TATGAAATTCAAAACCTTCCACCTGCCATGCTGCTTGCATTCCTGTGAGAAATCTTCTGTGG 780
QY	925 ACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGCGCATCTGGCCAC 984
DB	
	781 ACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGCGCATCTGGCCAC 840
QY	985 CAAGGAAATTCGACCCCTGACGATTACTCTTGACACTTTTATGTAATTCATTTGTTTATA 1044
DB	
	841 CAAGGAAATTCGACCCCTGACGATTACTCTTGACACTTTTATGTAATTCATTTGTTTATA 900

PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249219P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 PR 17-JAN-2001; 2001US-00764854.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM, Barash SC;
 DR P-PSDB; ADC46319.
 DR WPI; 2003-786918/74.
 XX
 PT New isolated human neoplastic disease-associated polypeptides and
 PT polynucleotides, useful for diagnosing, preventing, prognosticating or
 PT treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
 PT disease.
 XX
 PS Claim 1; SEQ ID NO 121; 302pp; English.
 XX
 CC The invention relates to one of 238 disclosed human neoplastic disease-
 CC associated polypeptides encoded by 171 disclosed cDNA sequences
 CC (including their domains, epitopes, full-length proteins, allelic variants
 CC or species homologues). Also included are there encoding nucleic acids, a
 CC recombinant vector comprising the nucleic acid, a recombinant host cell
 CC comprising the nucleic acid (expressing the protein), an isolated
 CC antibody that binds specifically to the isolated polypeptide, preventing,
 CC treating or ameliorating a medical condition, diagnosing a pathological
 CC condition or a susceptibility to a pathological condition in a subject,
 CC identifying a binding partner to the polypeptide, identifying an activity
 CC in a biological assay, and the gene corresponding to the cDNA sequence.
 CC The polypeptides, polynucleotides and antibodies are useful for
 CC detecting, preventing, diagnosing, prognosticating, treating or
 CC ameliorating medical conditions such as hyperproliferative diseases or
 CC cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
 CC systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
 CC or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
 CC anaemia or thrombocytopaenia), allergic reactions including asthma or
 CC eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
 Query Match 82.7%; Score 935.8; DB 10; Length 2156;
 Best Local Similarity 99.2%; Pred. No. 4.9e-255;
 Matches 951; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
 QY 146 CCATGGCGGCACAGACGCCGACGAGCCGACCAAGACAGCGACGACCTGCGCGACG 205
 DB 1 CCACGCGTCCGAGAGAGCGCCGACGAGCCGACCAAGACAGCGACGACCTGCGCGACG 60
 QY 206 AAGGGTTTGGGATGTAGCGTCTGCACCTTCAGAAACAGTGTGAGCCTTTAAATGCA 265

Db 61 AAGGGTTTGGGATGTAGCGTCTGCACCTTCAGAAACAGTGTGCTGAAGCCTTTAAATGCA 120
 QY 266 GCATCTGCATGTGAGGAAAGGCACCTCTCAACA-GAAAACCTCGGATCAATTCCTCAGCTG 324
 Db 121 GCATCTGCATGTGAGGAAAGGCACCTCTCAACCATTGAAACCTCGGATCAATTCCTCAGCTG 180
 QY 325 GTGGCACAACAAGTGGCACAACAAGTATGCCACCCACACCCCTCTAAAAGAGGAGAAG 384
 Db 181 GTGGCACAACAAGTGGCACAACAAGTATGCCACCCACACCCCTCTAAAAGAGGAGAAG 240
 QY 385 GAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAAGAGAAAATAGTCTCTAGT 444
 Db 241 GAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAAGAGAAAATAGTCTCTAGT 300
 QY 445 GTTACCAAGAAAATAACCAAGAAAACCAAGAAAACCAAGTCTGACATTCCTGAAAGATCCT 504
 Db 301 GTTACCAAGAAAATAACCAAGAAAACCAAGAAAACCAAGTCTGACATTCCTGAAAGATCCT 360
 QY 505 CCTAGTGAAGCAACAGCATACAGTCTGCAAAATGTACAAACAAAGACACGCGAAAACAAAT 564
 Db 361 CCTAGTGAAGCAACAGCATACAGTCTGCAAAATGTACAAACAAAGACACGCGAAAACAAAT 420
 QY 565 CACACCTCAAGGCCCGGCTGAAAAACGTGGACAGGACGACCTGCAACAGCAGTTGGCAGTA 624
 Db 421 CACACCTCAAGGCCCGGCTGAAAAACGTGGACAGGACGACCTGCAACAGCAGTTGGCAGTA 480
 QY 625 ACTGTGGCAACGTCACCGTCAATTCACAGACTTTAAGGAAAAGACTCGCTCTCATCG 684
 Db 481 ACTGTGGCAACGTCACCGTCAATTCACAGACTTTAAGGAAAAGACTCGCTCTCATCG 540
 QY 685 ACATCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACACAGACGAGCTCG 744
 Db 541 ACATCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACACAGACGAGCTCG 600
 QY 745 GGGTCAGAGACGACAGACAAGGGCTCTCTCCCGTTCTCCACGCCAAAGGGCGACATGTCA 804
 Db 601 GGGTCAGAGACGACAGACAAGGGCTCTCTCCCGTTCTCCACGCCAAAGGGCGACATGTCA 660
 QY 805 GCATCAATGATGAATCTTTGTGAAATTCACATGGAATTTGAAACCTATGATCAGG 864
 Db 661 GCATCAATGATGAATCTTTGTGAAATTCACATGGAATTTGAAACCTATGATCAGG 720
 QY 865 TATGAAATTCAAAACCTCCACCTGCGCTGCTTGCATCCCTGAGAGATCTTCTGTGG 924
 Db 721 TATGAAATTCAAAACCTCCACCTGCGCTGCTTGCATCCCTGAGAGATCTTCTGTGG 780
 QY 925 ACATCGACCTCTTAGTGATGTGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCAC 984
 Db 781 ACATCGACCTCTTAGTGATGTGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCAC 840
 QY 985 CAAGGAATTCGACCCCTGACGATTAATCTTGCACATTTTATGATATTCATTTTATATA 1044
 Db 841 CAAGGAATTCGACCCCTGACGATTAATCTTGCACATTTTATGATATTCATTTTATATA 900
 QY 1045 TGATTTTCTTAAACATCAATTAATTTGATGTGCTTGCATTAATCTACTTTTATAAAAA 1103
 Db 901 TGATTTTCTTAAACATCAATTAATTTGATGTGCTTGCATTAATCTACTTTTATAAAAA 959
 RESULT 11
 AAF55595
 ID AAF55595 standard; cDNA; 947 BP.
 XX AC AAF55595;
 XX DT 29-MAY-2001 (first entry)
 XX DE Nucleotide sequence of apoptin-associating protein 1 cDNA clone a.
 XX KW Apoptin-associating protein; AAP; apoptosis; cell proliferation;
 XX KW cell death; autoimmune disease; cancer; ss.
 XX OS Homo sapiens.

PD	07-MAR-2001.	107	TCATGATGAATCTTTGTCGAAATTCGACATGGAATTTGTGAAACTATGATGAATCAGGGTATG	868
XX				
PF	02-SEP-1999; 99EP-00202858.	624	TCATGATGAATCTTTGTCGAAATTCGACATGGAATTTGTGAAACTATGATGAATCAGGGTATG	863
XX				
PR	02-SEP-1999; 99EP-00202858.	869	AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGACAT	928
XX				
XX	(LEAD-) LEADD BV.	684	AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGACAT	743
XX				
DR	WPI; 2001-219813/23.	929	CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAAG	988
DR	P-PSDB; AAB67552, AAB67553, AAB67554, AAB67555, AAB67556, AAB67557, AAB67558.	744	CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAAG	803
XX				
PT	Novel isolated or recombinant apoptin-associating proteinaceous substance, apoptin-associating protein 1, useful for inducing apoptosis for treating cancer or autoimmune diseases caused by aberrant apoptosis.	989	GAATTCGACACCTGACGATTAATCTTTGACACTTTTATGATTTTATCCATCTGTTTATATGAT	1048
PT				
XX	Claim 4; Fig 1; 29pp; English.	804	GAATTCGACACCTGACGATTAATCTTTGACACTTTTATGATTTTATCCATCTGTTTATATGAT	863
XX				
PS		1049	TTTCTCTAACCAATCATTTATAATTTGGATGTCCTCGAATCTACTTTTAT-AAAAAGGCC	1107
XX				
CC	The present sequence encodes an apoptin-associating proteinaceous substance (apoptin-associating protein 1 (AAP-1)), which is capable of inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for inducing a p53-independent apoptosis. They are used for treating a disease where enhanced proliferation or decreased cell death is observed e.g. cancer or autoimmune disease. They are also used for diagnosis of diseases related with aberrations in the apoptotic process such as cancer and autoimmune diseases	864	TTTCTCTAACCAATCATTTATAATTTGGATGTCCTCGAATCTACTTTTATAAAAAGGCC	923
XX				
SQ	Sequence 947 BP; 309 A; 238 C; 198 G; 198 T; 0 U; 4 Other;	1108	TTGCTGGCCTCGAGAGATCTATGA	1131
	Query Match 77.9%; Score 881.4; DB 4; Length 947;			
	Best Local Similarity 97.6%; Pred. No. 9.4e-240;			
	Matches 902; Conservative 2; Mismatches 19; Indels 1; Gaps 1;			
QY	209 GGTTCGGATGTCGATGTCGACCTTCAGAACACAGTGTGAAAGCTTTAAATGACGA	268		
DB	24 GGAATTCGGATCTTCGAGGCCACGAGGCCGAAACAGTGTGAAAGCTTTAAATGACGA	83		
QY	269 TCTCGGATGTGAGAAAGGCACTCCACAGAAACCTCGGATCAATTTCTCAGCTGGTG	328		
DB	84 TCTCGGATGTGAGAAAGGCACTCCACAGAAACCTCGGATCAATTTCTCAGCTGGTG	143		
QY	329 CACAACAGTGGGACACAGTATGCCACCCACACCCCTTAAAAAGGAGAGAGAGA	388		
DB	144 CACAACAGTGGGACACAGTATGCCACCCACACCCCTTAAAAAGGAGAGAGAGA	203		
QY	389 AAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGAAATAGTCTTAGTGTTA	448		
DB	204 AAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGAAATAGTCTTAGTGTTA	263		
QY	449 CCAAGAAAATACCAACAGAAACCAACCAAGTCTGACATTTCTGAAGATCCTCCTTA	508		
DB	264 CCAAGAAAATACCAACAGAAACCAACCAAGTCTGACATTTCTGAAGATCCTCCTTA	323		
QY	509 GTGAAGCAACAGCATACAGTCTGCAATGCTCAACAAAGACGAGCAACAAATCACA	568		
DB	324 GTGAAGCAACAGCATACAGTCTGCAATGCTCAACAAAGACGAGCAACAAATCACA	383		
QY	569 CTTAAGGCCCGCTGAAAACGTTGACAGGAGCACTGCACAGCAAGTTGGCAGTAAGTG	628		
DB	384 CTTAAGGCCCGCTGAAAACGTTGACAGGAGCACTGCACAGCAAGTTGGCAGTAAGTG	443		
QY	629 TGGCAACGTCACGTCATTTATCAGACCTTTAAGGAAAGACTCGCTCTCATCGCAT	688		
DB	444 TGGCAACGTCACGTCATTTATCAGACCTTTAAGGAAAGACTCGCTCTCATCGCAT	503		
QY	689 CCTCATCCAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACCCAGACGAGCTCGGGGT	748		
DB	504 CCTCATCCAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACCCAGACGAGCTCGGGGT	563		
QY	749 CAGAGACACAGCAAGGGCTCTCTCCGTTCTTCCAGCCCAAGGGGCAATGTCAGCAG	808		
DB	564 CAGAGACACAGCAAGGGCTCTCTCCGTTCTTCCAGCCCAAGGGGCAATGTCAGCAG	623		

RESULT 13

AAF57184

ID AAF57184 standard; cDNA; 947 BP.

XX

AC AAF57184;

DT 29-MAY-2001 (first entry)

XX

DE Apoptin-associating protein (AAP)-1-a nucleotide sequence.

KW Apoptin-associating protein; AAP; apoptosis; p53; cell proliferation; cell death; cancer; autoimmune disease; cytostatic; immunosuppressive; gene therapy; AAP-1-a; ss.

XX

OS Homo sapiens.

XX

PN EP1083224-A2.

PD 14-MAR-2001.

XX

PF 01-SEP-2000; 2000EP-00203042.

XX

PR 02-SEP-1999; 99EP-00202858.

PR 21-OCT-1999; 99EP-00203465.

XX

PA (LEAD-) LEADD BV.

XX

PI Noteborn MHM, Danen-Van Oorschot AAM;

DR WPI; 2001-228257/24.

XX

PT New nucleic acids encoding apoptin-associating proteins capable of inducing p52 independent apoptosis, useful for treating a disease associated with enhanced cell proliferation or decreased cell death, e.g. cancer or autoimmune disease.

XX

PS Claim 6; Fig 1; 26pp; English.

CC

CC The invention provides isolated or recombinant nucleic acid (I), its functional encoding an apoptin-associating proteinaceous (AAP) substance capable of apoptosis. (I), the vector comprising (I), the host cell comprising the vector and the proteinaceous substance encoded by (I) are useful for inducing apoptosis, particularly p53-independent apoptosis, and for treating a disease where enhanced cell proliferation or decreased cell death is observed, such as cancer or an autoimmune disease. A composition comprising the nucleic acid or the AAP may further be used for diagnosing a disease related with aberrancies in the apoptotic process, and for detecting the presence of cancer cells or cells that are

Qy	702	GACCTCAGTGCAGGGTCAGAA	CAGCAGAGAAC	CCAGAGCAGCTCGGGGT	CAGAGCAGCA	GAGA	761
Db	188	GACCTCAGTGCAGGGTCAGAA	CAGCAGAGAAC	CCAGAGCAGCTCGGGGT	CAGAGCAGCA	GAGA	247
Qy	762	CNAGGGCTCCTCCGCTTCCT	CCAGGCCA	AGGGCGCATGTCAGCAGT	CAATGATGAATC	821	
Db	248	CNAGGGCTCCTCCGCTTCCT	CCAGGCCA	AGGGCGCATGTCAGCAGT	CAATGATGAATC	307	
Qy	822	TTTCTGAAATTCACATCGGAAT	TGTGAAAC	TATGAATCAGGGGTATGAAAT	TTCAAAACCT	881	
Db	308	TTTCTGAAATTCACATCGGAAT	TGTGAAAC	TATGAATCAGGGGTATGAAAT	TTCAAAACCT	367	
Qy	882	CCACTGCCCATGTGCTTGTCAT	CCCTGGAGAA	TCTTCTGTGGACATCGACCT	TTTAGTG	941	
Db	368	CCACTGCCCATGTGCTTGTCAT	CCCTGGAGAA	TCTTCTGTGGACATCGACCT	TTTAGTG	427	
Qy	942	ATGCTGCCAGGATAAATTTCTG	CTTTGCCATG	GGGCATCTTGGCCACA	CAAGGAATTTGCGACCC	1001	
Db	428	ATGCTGCCAGGATAAATTTCTG	CTTTGCCATG	GGGCATCTTGGCCACA	CAAGGAATTTGCGACCC	487	
Qy	1002	TGACGATTACTCTTG	1016				
Db	488	TGACGATTACTCTTG	502				

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Job time : 697.404 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 07:52:31; Search time 4310.65 Seconds
(without alignments)
9987.065 Million cell updates/sec

Title: US-09-655-109A-5
Perfect score: 1131
Sequence: 1 tataactatcattgatga.....tggcctcgagagatcatga 1131

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	862.2	76.2	895	CK230944	ILLUMIGEN
2	855.4	75.6	1436	AK033024	Mus muscu
3	826.8	73.1	932	AJ816315	AJ816315
4	726.2	64.2	799	CK774847	963641 MA
5	708.6	62.7	736	BM985193	UT-CF-EC1
6	691.4	61.1	906	BI553612	603190533
7	672.6	59.5	936	BE300021	600944142
8	671.8	59.4	707	EX924636	BX924636
9	668.6	59.1	798	BU704183	602749436
10	659.2	58.3	870	BG827273	964031 MA
11	656.4	58.0	726	CK777039	964031 MA
12	652.4	57.7	654	AY400131	Homo sapi
13	645.2	57.0	662	BQ015219	UT-H-ED1-
14	634	56.1	664	CK299391	UT-E-EJ1-
15	628	55.5	650	BQ189224	UT-E-EJ1-
16	616.4	54.5	642	BF116048	7n76908.x
17	612	54.1	621	AI627241	ty72a11.x
18	607.6	53.7	1074	BQ053013	AGENCOURT
19	607.2	53.7	1077	BI114501	602862192
20	605.6	53.5	792	CK533672	UT-M-HO-
21	603.8	53.4	718	CK636066	UT-M-HO-
22	603.2	53.3	784	CK635466	UT-M-HNO-
23	591.4	52.3	769	CA324092	UT-M-FY-
24	588.4	52.0	948	CG494853	OST33953

25	583.6	51.6	654	9	AY400133	AY400133
26	583.6	51.6	751	6	CB724087	UI-M-FY0-
27	578.4	51.1	745	6	CD355761	UI-M-FY0-
28	577	51.0	639	6	CB444669	695860 MA
c	574	50.8	618	4	BM312863	BM312863
29	572.8	50.6	723	7	CM457401	UI-M-HNO-
30	569.6	50.4	608	4	BI345349	737146 MA
31	569.4	50.3	573	1	AI693196	wd68f05.x
c	568.4	50.3	610	6	CB287220	CMD55_C02
32	568.4	50.3	573	1	AI912660	we12c06.x
33	549.8	48.6	573	1	AI912660	CMD55_C09
34	549	48.5	589	6	CB287224	CMD55_C09
35	548.8	48.5	589	6	CB461283	721237 MA
36	548.8	48.5	589	6	CB461283	721237 MA
c	545.4	48.2	548	2	AW193683	xm23d02.x
c	544.4	48.1	576	1	AI693651	wd79f12.x
c	543.4	48.0	564	6	CB854840	UI-CF-EC1
c	541.4	47.9	703	7	CK639892	UI-M-HNO-
40	541.4	47.9	703	7	CK639892	UI-M-HNO-
41	541.4	47.9	703	7	CK639892	UI-M-HNO-
42	540	47.7	814	9	CG498682	OST40156
43	539.4	47.7	700	7	CK640200	UI-M-HNO-
c	538	47.6	547	1	AA725613	ai19d09.8
44	537	47.5	545	7	CV029042	7711 Full

ALIGNMENTS

RESULT 1
CK230944
LOCUS ILLUMIGEN MCQ_1331 Katze MMLP2 Macaca mulatta cDNA 5' similar to human RYBP (Hs.7910), mRNA sequence.
DEFINITION CK230944.1 GI:39637302
ACCESSION CK230944
VERSION EST.
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE Macaca mulatta
ORGANISM Macaca mulatta
REFERENCE 1 (bases 1 to 895)
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness
Illumigen Biociences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.10.17, 765 Q20 bases. Assemblies in contig w/ 1 member(s). Contig contains 1 (0%) lib members.
PCR Primers
FORWARD: CCTCACTAAAGGGACAAA
BACKWARD: CACTATAGGGCGAATGGTA
Insert Length: 895 Std Error: 0.00
Plate: CL000013 row: C column: 06
Seq primer: CCTCACTAAAGGGACAAA
POLYA=Yes.
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/note="Organ: placenta; Vector: Uni-ZAP XR; Site 1: ECOR I; Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis kit (catalog #200400) and ZAP-cDNA Gigapack III Gold Cloning Kit (Catalog #200450)"

ORIGIN

Query Match	76.2%;	Score	862.2;	DB	7;	Length	895;
Best Local Similarity	99.1%;	Pred.	No. 1.8e-223;				
Matches	867;	Conservative	0;	Mismatches	23;	Indels	0;
Gaps	0;						
Qy	229	TGCACCTTCAGAAAACAGTCTGTAAGCCCTTTAAATGCAGCATCTGGATGTGAGGAAAGGC	288				
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Qy	289	ACCTCCACCAGAAAACCTCGGATCAATTTCTCAGCTGGTGGCACAAACAAAGTGGCCACACAG	348				
Db	61	ACCTCCACCAGAAAACCTCGGATCAATTTCTCAGCTGGTGGCACAAACAAAGTGGCCACACAG	120				
Qy	349	TATGCCACCCACACCCCTTAAAGAGAGAAAGGAGAAAGTTGAAAACGACGACAAA	408				
Db	121	TATGCCACCCACACCCCTTAAAGAGAGAAAGGAGAAAGTTGAAAACGACGACAAA	180				
Qy	409	GAGAAACCTTGAGAAAGACAGGAATTTAGTCTCTAGTGTTCACAGAAAATACCAACAAG	468				
Db	181	GAGAAACCTTGAGAAAGACAGGAATTTAGTCTCTAGTGTTCACAGAAAATACCAACAAG	240				
Qy	469	AAAAACCAACCAAGCTGTGACATTTCTGAAAGATCTCTCTAGTGAAGCAAAACAGCATACAG	528				
Db	241	AAAAACCAACCAAGCTGTGACATTTCTGAAAGATCTCTCTAGTGAAGCAAAACAGCATACAG	300				
Qy	529	TCTGCAATGTCTAACAAAGACACGAGCAAAACATACACCTCAAGGCCCGGCTGAAA	588				
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Qy	589	AACGTGGACAGGACACTGCACAGAGTTGGCAGTAAGTGTGGGCAACGTCACCGTCAAT	648				
Db	361	AACGTGGACAGGACACTGCACAGAGTTGGCAGTAAGTGTGGGCAACGTCACCGTCAAT	420				
Qy	649	ATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACATCTCTATCCACAGTGAACCTCC	708				
Db	421	ATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACATCTCTATCCACAGTGAACCTCC	480				
Qy	709	AGTCAGGTCAGACAGACAGACAGACAGCTCGGGTCAGAGACAGACAGACAGGC	768				
Db	481	AGTCAGGTCAGACAGACAGACAGACAGCTCGGGTCAGAGACAGACAGACAGGC	540				
Qy	769	TCCTCCGCTCTCCACGCAAGGGGACATGTCCAGCAGTCAATGATGAATCTTTGTGA	828				
Db	541	TCCTCCGCTCTCCACGCAAGGGGACATGTCCAGCAGTCAATGATGAATCTTTGTGA	600				
Qy	829	AATTCACATGGAATTTGAAACATATGAATCAGGGTATGAAATTCAAAACCTCCACCTG	888				
Db	601	AATTCACATGGAATTTGAAACATATGAATCAGGGTATGAAATTCAAAACCTCCACCTG	660				
Qy	889	CCATGCTGCTTGCATCCCTGGAGAACTCTCTGTGGACATCGACCTCTTAGTGATGCTGC	948				
Db	661	CCATGCTGCTTGCATCCCTGGAGAACTCTCTGTGGACATCGACCTCTTAGTGATGCTGC	720				
Qy	949	CAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAAGGAATTTTCGACCCCTGCAGAT	1008				
Db	721	CAGGATAATTTCTGCTTGCATGGGCATCTGGCCACCAAGGAATTTTCGACCCCTGCAGAT	780				
Qy	1009	TACTCTTGACATTTTATGTATTCATCTGTTTATATGATTTTCTTAACAATCATTTATA	1068				
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Qy	1069	ATTGATGTGCTCCTGAATCTACTTTTTATAAAAA	1103				
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RESULT 2
AK033024
LOCUS
DEFINITION
Mus musculus 11 days embryo gonad cDNA, RIKEN full-length enriched library, clone:7030405H07 product:RING1 and YY1 binding protein, full insert sequence.
AK033024

AK033024.1 GI:26328784
HTC; CAP trapper.
Mus musculus (house mouse)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1436)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES		Location/Qualifiers	
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	Matches 939;	Conservative 0;	Mismatches 81; Indels 5; Gaps 3;
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QY	139	TCATGACCATGGGCGACAGAGAGCCGACGCGCCAAAAGACACAGCGAAACCTGC	198
Db	118	TCCATGACCATGGGCGACAGAGAGCCGACGCGCCAAAAGACACAGCGAAACCTGC	177
QY	199	GCAGCGAAGGGTTTGGGATTTAGCGTCTGCACCTTCAGAAAACAGTCTGAAGCCTT	258
Db	178	GCAGCGAAGGGTTTGGGATTTAGCGTCTGCACCTTTAGGACAGCGCCGAGCCCTT	237
QY	259	AAATGACGATCTGCGATGTGAGGAAGGCACCTCCACAGAAAACCTCGGATCAATCT	318
Db	238	AAATGACGATCTGCGATGTGCGAAGGACCTCCACAGAAAACCTCGCATCAATCT	297
QY	319	CAGCTGGTGCAACAAGTGGCAACAAGTATGCGACCCGCCACCCCTTAAAGGAG	378
Db	298	CAGCTGGTGCGACAGAGTGGCACAGTAGTAGCGCACTCCACCTCCCTTAAGAGGAG	357
QY	379	AGAAGGAGAACTTCAAAGCAGGACAAAGAGAACTTGAGAAAGACAAAGAAATAGT	438
Db	358	AGAAGGAGAACTTCAAAGGCTGCAAGAAAGCTGCAAGAAAGCCAGAGAACAGCATAGC	417
QY	439	CCTAGTGTACCAAGAAAATACCAACAAGAAAACCAAAACCAAGTCTGACATTCGAAA	498
Db	418	CCCAGTGTACCAAGAAAACCAACAAGAAAACCAAAACCAAGTCTGATATTCGAAA	477
QY	499	GATCCTCTAGTGAAGCAACAGCATACAGTCTGCAATGCTTACACAAAGCCAGCGAA	558
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QY	559	ACAAATACACACCTCAAGGCCCGGCTGAAAACCTGCAAGAGGACACTGCACAGCAGTTG	618
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QY	679	TCATCGACATCTCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAAACAGACGAAACGAGC	738
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QY	739	AGCTCGGGTTCAGAGACGACAGAAAGGCTCCCGTTCCTCCAGCCCAAGAGGGCGAC	798
Db	718	AGCTCGGGTTCAGAGACGACAGAAAGGCTCCCGTTCCTCCAGCCCAAGAGGGCGAC	777
QY	799	ATGTGACAGTCAATGATGAATCTTTGTGAAATTCACATGCAATTTGTGAAAACCTATGAA	858
Db	778	ATGTGACAGTCAATGATGAATCTTTGTGAAATTCACATGCAATTTGTGAAAACCTATGAA	836
QY	859	TCAGGGTATGAAATTCAAAACCTCCACCTGCCCCATGCTGCTGCAATCCCTCGAGAACTCT	918
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QY	919	CTGTGGACATCGACCTCTTAGTGATGCTGCGCAGGATAATTTCTGCTTGGCCATGGCATCT	978
Db	896	CTGTGGA---CGACCTTTGTAGTGACGCTACAGAGAGGTTCCGCTTGCCGTGGGCATCT	952
QY	979	GGCCACCAAGGAAATTCGCACCTCGACGATTACTCTTGACACTTTTATGTATTCATTTGT	1038
Db	953	GGCTACCAAGGAAATTCGTACCTCGACGATTACTCTTGACACTTTTATGTATTCATTTGT	1012
QY	1039	TTTATATGATTTTCTTAACATCAATTTATATATTTGATGTGCTCTCGAATCTACTTTTAT	1098
Db	1013	TTTATATGATTTTCTTAACATCAATTTATATATTTGATGTGCTCTCGAATCTACTTTTAT	1072
QY	1099	AAAAA 1103	
Db	1073	ATATA 1077	
RESULT 3			
LOCUS	AJ816315	932 bp	mRNA linear EST 13-SEP-2004
DEFINITION	AJ816315	KN206 Bos sp.	cDNA clone C0005210111, mRNA sequence...
ACCESSION	AJ816315		
VERSION	AJ816315.1	GI:51883791	
KEYWORDS	EST.		
SOURCE	Bos sp.		
ORGANISM	Bos sp.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
	Bovinae; Bos.		
REFERENCE	1 (bases 1 to 932)		
AUTHORS	McGuire, K. and Glass, B.J.		
TITLE	Unpublished ESTs, McGuire and Glass		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: McGuire K		
	Genomics and Genetics		
	Roslin Institute		
	Roslin, Midlothian, EH25 9PS, UNITED KINGDOM		
	Single pass sequencing. Bases called and trimmed with phred		
	v0.020425.c. Vector identified by cross_match with the -minscore 20		
	and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site		
	1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library		
	constructed from pooled monocytes from Bos taurus (Holstein) and		
	Bos indicus (Sahiwal) cattle subjected to various stimuli, and		
	including infection with the protozoan parasite Theileria annulata.		
FEATURES	Location/Qualifiers		
	1..932		
source	/organism="Bos sp."		
	/mol_type="mRNA"		
	/db_xref="taxon:29061"		
	/clone="C0005210111"		
	/tissue_type="blood"		
	/cell_type="bovine monocyte"		
	/clone_lib="KN206"		
	/note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);		
	Site_2: NotI; Normalised library constructed from pooled		
	monocytes from Bos taurus (Holstein) and Bos indicus		

(Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite *Theileria annulata*"

ORIGIN	Query Match	73.1%	Score 826.8	DB 1	Length 932
	Best Local Similarity	95.2%	Pred. No. 8e-214		
	Matches 874	Conservative 0	Mismatches 42	Indels 2	Gaps 2
Qy	187	GCAGAACTCGCGCAGACGAAGGGTTTTGGGATTGTAGCGTCTGCACCTTCAGAAACAGT	246		
Db	1	GCAAAACCTCGCGCAGACGAAGGGTTTTGGGATTGTAGCGTCTGCACCTTCAGAAACAGC	60		
Qy	247	GCTGAAGCCCTTTAAATGCAGCATCTGCGATGTGAGGAAAGGCACCTCCACGAGAAACCT	306		
Db	61	GCCGAGCCCTTTAAATGCAGTATCTGCGATGTGGAAGAGGCACCTCCACGAGAAACCT	120		
Qy	307	CGGATCAATTTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGGCAACACCCCAACCC	366		
Db	121	CGGATCAATTTCCAGCTGGTGGCAACAAGTGGCCACGCAAGTGGCCACGAGTATGCCATCCACCAACC	180		
Qy	367	CCTAAAGAGAGAGAGGAGAAAGTTGAAAGCAGGACACAGAGAAACCTGAGAAAGAC	426		
Db	181	CCTAAAGAGAGAGAGGAGAAAGTTGAAAGCAGGACACAGAGAAACCTGAGAAAGAT	240		
Qy	427	AAGGAAATTAGTCTCTAGTGTGTACCAAGAAATAACCAAGAAACCAACCAAAAGTCT	486		
Db	241	AAAGAAATTAGTCTCTAGTGTACCAAGAAATAACCAAGAAACCAACCAAAAGTCT	300		
Qy	487	GACATTTCTGAAGATCTCTCTAGTGAAGCAACAGCATACAGTCTGCAATATGTCACACA	546		
Db	301	GATATTTCTGAAGATCTCTCTAGTGAAGTGAACAGTATACAGTCTGCAATATGTCACACA	360		
Qy	547	AAGACCAAGCAACCAATCAACCTCAAGCCCGGCTGAAACAGTGAACAGGACGAGCACT	606		
Db	361	AGACCAAGTGAACCAATCAACCTCAAGCCCGGCTGAAACAGTGAACAGGACGAGCACT	420		
Qy	607	GCACAGCAGTTGGCAGTAACTGTGGGCAACGCTCAACGTCATTTATCACAGACTTTAAGGAA	666		
Db	421	GCACAGCAGTTGGCAGTAACTGTGGGCAACGCTCAACGTCATTTATCACAGACTTTAAGGAA	480		
Qy	667	AAGACTCGCTCCTCATCGACATCCTCATCCACAGTGACCTCCAGTGCAGGCTCAGAACAG	726		
Db	481	AAGACTCGCTCCTCCTCGACATCCTCATCCACAGTGACCTCCAGTGCAGGCTCAGAACAG	540		
Qy	727	CAGAACCAAGCAGCTCGGGGTGAGAGACACAGAACAGGCGCTCTCCCGTCTCTCCACG	786		
Db	541	CAGAACCAAGCAGCTCGGGGTGAGAGACACAGAACAGGCGTCTCTCCCGTCTCTCCACG	600		
Qy	787	CCAAAGGGGACATGTGAGCAGTCAATGATGAATCTTTGTGAAATTGCACATGGAATTGT	846		
Db	601	CCAAAGGGGACATGTGAGCAGTAAATGATGAGTCTTTCTGAAAGTTGCACATGGAATTGT	660		
Qy	847	GAAACTATGAATCAGGATGAAATTCAAAACCTCCACCTGCCCTGCTGCTTGCA-TC	905		
Db	661	GAAACTATGAATCAGGATGAAATTCAGTCTCTCCACCTGCCCTGCTGCTTGCAACCC	720		
Qy	906	CCTGGGAAATCTTCTGTGGACATCGACCTCTTAGTGTAGTGTGCGAGGATTAATTTCTGCTT	965		
Db	721	CCTGGGAAATCTTCTGTGGACATCGACCTCTTAGTGTAGTGTGCGAGGATTAATTTCTGCTT	780		
Qy	966	GCCATGGGCATCTGGCCACCAAGAAATTTGCGACCTTGACGATTACTCTTGACACTTTTA	1025		
Db	781	GCCATGGGCATCTGGCCACCAAGAAATTTGCGACCTTGACGATTACTCTTGACACTTTTA	840		
Qy	1026	TGTATTCATTTGTTTATATGATTTTCTTAACATCATTTATTAATTCGATGTGCTCTCTGA	1085		
Db	841	TGTATTCATTTGTTTATATGATTTTCTTAAC-ATCATTTTAAATTCGATGTGCTCTCTGA	899		
Qy	1086	ATCTACTTTTATAAAAA 1103			
Db	900	ATCTACTTTTATAAAAA 917			

RESULT 4	CK774847	799 bp	mRNA	linear	EST 20-FEB-2004
LOCUS	963641 MARC 2BOV Bos taurus cDNA 3', mRNA sequence.				
DEFINITION	CK774847				
ACCESSION	CK774847.1	GI:42728990			
VERSION	EST.				
KEYWORDS	Bos taurus (cow)				
SOURCE	Bos taurus				
ORGANISM	Bos taurus				
REFERENCE	Bos taurus				
AUTHORS	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahnenkrug, S.C., Bennett G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Partea, G., Holt, I., Karanycheva, S., Liang, F., Quackenbush, J., and Keele, J.W.				
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle				
JOURNAL	Genome Res. 11 (4), 626-630 (2001)				
MEDLINE	21180013				
PUBMED	11282978				
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_malt option. Vector identified with cross match v0.990329. Plate: 105 row: P column: 12 Seq primer: GTAATACGACTCACTATAGG. Location/Qualifiers 1. .799 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone_lib="MARC 2BOV" /notes="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."				
FEATURES	source				
ORIGIN	Query Match 64.2%; Score 726.2; DB 7; Length 799; Best Local Similarity 95.1%; Pred. No. 2e-186; Matches 760; Conservative 0; Mismatches 38; Indels 1; Gaps 1;				
Qy	301 AAACCTCGGATCAATTCTCAGCTGGTGGCAACAAGTGCACACAGTAGTATGCCACCCCA 360				
Db	799 AAACCTCGGATCAATTCTCCAGCTGGTGGCAGCAGTGGCCCCAGCAGTAGTATGCCACTCCA 740				
Qy	361 CCACCCCTAAAGGAGAGAGAGGACAAAGTTGAAAAGCAGGACGAAGAAGAACTCTGAG 420				
Db	739 CCACCCCTAAAGGAGAGAGAGGAGAAAGTTGAAAACAGCAAGCAAGAACTCTGAG 680				
Qy	421 AAAGACAAGGAAATTTAGTCTCTAGTGTGTACCAAGAAAAAATACCAACAAGAAAAACCAACCA 480				
Db	679 AAAGATAAGAAATTTAGTCTCTAGTGTTCACCAAGAAAAAATACCAACAAGAAAAACCAACCA 620				
Qy	481 AAGTCTGACATTCGAAAGATTCCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCT 540				
Db	619 AAGTCTGATATTCGAAAGATTCCTCTCTAGCGAAGTGAACATGATACAGTCTGCAAAATGCT 560				
Qy	541 ACACAAAGACACGAGCAAAACAATACACACTCAAGGCCCGCGCTGAAAAACGTGCACAGG 600				
Db	559 ACACAAAGACACAGTGAACGAATACACACTCAAGGCCCGCGCTGAAAAACGTGCACAGG 500				
Qy	601 AGCACTGCACAGCAGTTGGCAGTAACCTGTGGGCAACGCTCACCGCTCAITATTACACAGACTTT 660				


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Db 186 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTGCCATGGGCATCTGGCCACCAAG 127
QY 989 GAAATTCGACCTGACGATTTACTCTTGACACTTTTATGTATTCATTTGTTTATATGAT 1048
Db 126 GAAATTCGACCTGACGATTTACTCTTGACACTTTTATGTATTCATTTGTTTATATGAT 67
QY 1049 TTTCCTAACAAATCAATTTAATTTGATGTGCTTCCTGAATCTACTTTTATATAAAA 1103
Db 66 TTTCCTAACAAATCAATTTAATTTGATGTGCTTCCTGAATCTACTTTTATATAAAA 12

RESULT 6
B1553612 906 bp mRNA linear EST 05-SEP-2001
LOCUS 603190533F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261840 5',
DEFINITION mRNA sequence.
ACCESSION B1553612
VERSION B1553612.1 GI:15440924
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11660 row: a column: 09
High quality sequence stop: 742.
Location/Qualifiers
1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5261840"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dr primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN
Query Match 61.1%; Score 691.4; DB 4; Length 906;
Best Local Similarity 97.9%; Pred. No. 6.4e-177;
Matches 753; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

QY 75 CCACGAAGCCCTTCTCTCCAGCGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 134
Db 24 CCGGACGCGGTTCTCTCTCCAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 83
QY 135 CCATCCATGACATGGGGGACAGAGAGCCCGACCGCCGCAAAAAGACAGCGAAACC 194
Db 84 CCCATCCATGACATGGGGGACAGAGAGCCCGACCGCCGCAAAAAGACAGCGAAACC 143
QY 195 TGCCCGCAGACGAAGGGTTTTGGGATTGTAGCGTCTGCACCTTCAGAAAACAGTGTGAAGC 254
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Db 144 TGCCCGCAGACGAAGGGTTTGGGATTGTAGCGTCTGCACCTTCAGAAAACAGTGTGAAGC 203
QY 255 CTTTAAATGCAAGCATCTCGGATGTGAGAAAGGACCTCCACGAGAAAACCTCGGATCAA 314
Db 204 CTTTAAATGCAAGCATCTCGGATGTGAGAAAGGACCTCCACGAGAAAACCTCGGATCAA 263
QY 315 TTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGCCACCCCTTAAAAA 374
Db 264 TTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGCCACCCCTTAAAAA 323
QY 375 GGAGAAGAAGGAGAAAAGTTGAAAAGCAGGACAAAAGAGAAAACCTGAGAAAACAAGGAAT 434
Db 324 GGAGAAGAAGGAGAAAAGTTGAAAAGCAGGACAAAAGAGAAAACCTGAGAAAACAAGGAAT 383
QY 435 TAGTCTTAGTGTGTACCAAGAAAATAACCAACAAGAAAACCAAAACCAAGTCTGACATTCT 494
Db 384 TAGTCTTAGTGTGTACCAAGAAAATAACCAACAAGAAAACCAAAACCAAGTCTGACATTCT 443
QY 495 GAAAGATCCTCTAGTGAAGCAACACAGCATACAGTCTGCAAAATGCTCAACAAAAGACCGAG 554
Db 444 GAAAGATCCTCTAGTGAAGCAACACAGCATACAGTCTGCAAAATGCTCAACAAAAGACCGAG 503
QY 555 CGAAACAAATCACACACCTCAAGGCCCGCGCTGAAAACGTTGGACAGGAGCACTGCACAGCA 614
Db 504 CGAAACAAATCACACACCTCAAGGCCCGCGCTGAAAACGTTGGACAGGAGCACTGCACAGCA 563
QY 615 GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATACAGACTTTAAGGAAAAGACTCG 674
Db 564 GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATACAGACTTTAAGGAAAAGACTCG 623
QY 675 CTCCTCATCGACATCTTCATCC-ACAGTGACCTCCAGTGAGGGTTCAGAACAGCAGAGAAC 733
Db 624 CTCCTCATCGACATCTTCATCC-ACAGTGAGCTCCAGTGAGGGTTCAGAACAGCAGAGAAC 683
QY 734 AGACGAGCTCGGGGTTCAGAGACAGCA-CAAGGGCTCTCTCCCGTTCT-CCACGCCAAA 791
Db 684 AGACGAGCTC-GGGTTCAGAGACAGCAGACCAAGGGCTCTCTCCCGTTCTCTCCACGCCAAA 742
QY 792 GGGGACATGTACAGCTCAATGATGATCTTTGTGAATTCACATGG 840
Db 743 GGGGACATGTACAGCTCAATGATGATCTCTCTGACATTTGCCCTTGG 790

RESULT 7
B1553612 936 bp mRNA linear EST 20-JUL-2000
LOCUS 60944142F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960195 5',
DEFINITION mRNA sequence.
ACCESSION B1553612
VERSION B1553612.1 GI:9183769
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 936)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM53 row: c column: 12
High quality sequence stop: 713.
Location/Qualifiers
1..936
/organism="Homo sapiens"

FEATURES
source
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/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:2960195"
/clisue_type="Znabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 17"
/site="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8Kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

Query Match 59.5%; Score 672.6; DB 2; Length 936;
Best Local Similarity 93.3%; Pred. No. 8.6e-172;
Matches 770; Conservative 0; Mismatches 44; Indels 11; Gaps 6;

QY 75 CCACGAGGCTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGTACAG 134
DB 67 CCGGACGGCGTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGTACAG 126
QY 135 CCATCCATGACATGGGCGCAAGAAGAGCCGACCGCCGCAAAAGACGCGAAACC 194
DB 127 CCATCCATGACATGGGCGCAAGAAGAGCCGACCGCCGCAAAAGACGCGAAACC 186
QY 195 TCCCGCAGACGAAGGTTTGGATTTGTAGCTTGTGACCTTCAGAACAGTGTGAAGC 254
DB 187 TCCCGCAGACGAAGGTTTGGATTTGTAGCTTGTGACCTTCAGAACAGTGTGAAGC 246
QY 255 CTTTAAATCAGCATCTGGATGTGAGGAAGGCACTCCACGAGAAACCTCGATCAA 314
DB 247 CTTTAAATCAGCATCTGGATGTGAGGAAGGCACTCCACGAGAAACCTCGATCAA 306
QY 315 TTCTCAGCTGTGGCAACAAGTGGCAACAAGTATGCCACCCACACCCCTTAAAAA 374
DB 307 TTCTCAGCTGTGGCAACAAGTGGCAACAAGTATGCCACCCACACCCCTTAAAAA 366
QY 375 GGAGAGAGAGGAAAGTTGNAAGCAGGACCAAGAGAACTGTGAGAAAGACAAGGAAT 434
DB 367 GGAGAGAGAGGAAAGTTGNAAGCAGGACCAAGAGAACTGTGAGAAAGACAAGGAAT 426
QY 435 TAGTCTAGTGTACCAAGAAAATACCAAGAAAACCAAGAAAACCAAGTCTGACATCT 494
DB 427 TAGTCTAGTGTACCAAGAAAATACCAAGAAAACCAAGAAAACCAAGTCTGACATCT 486
QY 495 GAAAGATCTCTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAAGACCAAG 554
DB 487 GAAAGATCTCTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAAGACCAAG 546
QY 555 CGAAACAAATACACCTCAAGGCCCGGCTGAAAAACGTGGACAGGACACTGCAAGCA 614
DB 547 CGAAACAAATACACCTCAAGGCCCGGCTGAAAAACGTGGACAGGACACTGCAAGCA 606
QY 615 GTTGGCAGTAACCTGTGGGCAACGTACCGTCTATTATCAGAGCTTTAAG-GAAGAGCTC 673
DB 607 GTTGGCAGTAACCTGTGGGCAACGTACCGTCTATTATCAGAGCTTTAAGTGAAGAGCTC 666
QY 674 GCTCCTCATCGACATCTCATCCACAGTGCACCTCCAGTGCAGGCTCAGAACGAGAAC 733
DB 667 GCTCCTCATCGAATCTCATCCACAGTGCACCTCCAGTGCAGGCTCAGAACGAGAAC 725
QY 734 AGAGCAG- ---CTCGGGGTGAGAGACACAGCAA- GGGCTCTCTCCCGTTCTCCAGCC 788
DB 726 AGAGCAGCATACTCGGGGTCCAGAGAGACACAGCAAGGGGCTCTCCCGTCTCTCCAGCC 785
QY 789 AAGGGGGAATGT- ---CAGCAGTCAATGATGAATCTTTGTGAAATGACATGGAAATTG 845
DB 786 AATGGGCGCAACATGTCAAGCAGCTCATGATGAATCTTCTGGAAATTGGCAATTG 845
QY 846 TGAAACTAGATCAGGGTATGAAATTCAAACCTCCACCTGCC 890

846 TG-ACACTATGAATCCGGGAATTGAACTCCAGACACAACTGCC 899

RESULT 8
BX924636
LOCUS
DEFINITION
BX924636 Sus Scrofa library (scan) Sus scrofa cDNA clone
scan0017d.d.20 5prim, mRNA sequence.
ACCESSION
BX924636
VERSION
BX924636.1 GI:41141484
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 707)
AUTHORS
Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
Soares,M., Bonaudo,F. and Hately,F.
TITLE
A Pig Normalised Multi-Tissue cDNA Library
JOURNAL
Unpublished (2003)
COMMENT
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0017 row: d column: 20.
Location/Qualifiers
1..707
/organism="Sus scrofa"
/mol_type="mrna"
/db_xref="taxon:9823"
/clone="scan0017d.d.20"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/clone_lib="Sus Scrofa library (scan)"
/note="tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adnais, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Query Match 59.4%; Score 671.8; DB 5; Length 707;
Best Local Similarity 96.9%; Pred. No. 1.3e-171;
Matches 685; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 391 GTTGAAGAGCAGGACCAAGAGAAACCTGAGAAAGCAAGGAATTTAGTCTAGTGTACC 450
DB 1 GTTGAAGAGCAGATTAAGAGAAACCAAGAGAAAGATAAGGAATTTAGTCTAGTGTACC 60
QY 451 AAGAAAAATACCAACAGAAAAACCAAGTCTGACATTTCTGAAGATCTCTTAGT 510
DB 61 AAGAAAAATACCAACAGAAAAACCAAGTCTGATTTCTGAAGATCCACTAGT 120
QY 511 GAAGCAACAGCATACAGTCTGCAAAATGCTACAAAGACGAGCAATCAACATCACACC 570
DB 121 GAAGCAACAGCATACAGTCTGCAAAATGCTACAAAGACGAGCAATCAACATCACACT 180
QY 571 TCAAGGCCCCGCTGAAAAACCGTGACAGGAGCACTGCACAGAGTTGGCAGTAACGTGTG 630
DB 181 TCAAGGCCCCGCTGAAAAACCGTGACAGGAGCACTGCACAGAGTTGGCAGTAACGTGTG 240
QY 631 GGCACAGTCACCGTCAATTATCAAGCTTTAAGGAAAAAGACTCGCTCTCATCGACATCC 690

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Db      241  GGCACGTCACGTCATTATCACAGACTTTAAGGAABAGACTCGCTCTCTCGACATCC 300
Qy      691  TCATCCACAGTGAACCTCCAGTGCAGGGTCAGAACAGCAGACAGAGCAGCTCGGGGTCA 750
Db      301  TCATCCACAGTGAACCTCCAGTGCAGGGTCAGAACAGCAGACAGAGCAGCTCGGGGTCTG 360
Qy      751  GAGACACAGACAAGGGTCTCCCGTTCCCTCCAGCCCAAGGGGGCAGATGTCAGCAGTC 810
Db      361  GAGACACAGACAAGGGTCTCCCGTTCCCTCCAGCCCAAGGGGGCAGATGTCAGCAGTA 420
Qy      811  AATGATGAATCTTTGTGAAATGACATGGAATTTGTGAAATCTAATGAATCAGGGTATGAA 870
Db      421  AATGATGAATCTTTGTGAAATGACATGGAATTTGTGAAATCTAATGAATCAGGGTATGAA 480
Qy      871  ATTCAAAACCTCCACTGCGCCCATGCTGTGTGATCCCTGGAGAAATCTTCTGTGACATCG 930
Db      481  ATTCAATCTCCACTGCGCCCATGCTGTGTGATCCCTGGAGAAATCTTCTGTGACATCG 540
Qy      931  ACCTCTTAGTGTGCTGCCAGGATATTTCTGCTGCCATGGCATCTGGCCACCAAGGA 990
Db      541  ACCTCTTAGTGTGCTGCCAGGATATTTCTGCTGCCATGGCATCTGGCCACCAAGGA 600
Qy      991  ATTTCCGACCCCTGACGATCTCTTGACACATTTTATGTATTCATTTGTTTATATGATTT 1050
Db      601  ATTTCCGACCCCTGACATTTACTCTTGACACATTTTATGTATTCATTTGTTTATATGATTT 660
Qy      1051 TCCTAACCAATCATTTATTAATGGATGCTGCTCTGAAATCTACTTTTATA 1097
Db      661  TCCTAACCAATCATTTATTAATGGATGCTGCTCTGAAATCTACTTTTATA 707
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RESULT 9
BU704183
LOCUS   BU704183
DEFINITION UI-M-FOO-bzs-c-01-0-UI_r1 NIH BMAP_F00 Mus musculus cDNA clone
IMAGE:6406584 5', mRNA sequence.
ACCESSION BU704183
VERSION   BU704183.1
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 798)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Jim Lin, University of Iowa
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
```

```
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 38-78, >GC_rich#Low_complexity
Seq primer: pYX-5,
Location/Qualifiers
1..798
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6406584"
/tissue_type="whole brain"
/dev_stages="embryo 12.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_F00"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
```

FEATURES

source

Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGACC. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

```
Query Match      59.1%; Score 668.6; DB 5; Length 798;
Best Local Similarity 91.6%; Pred. No. 1e-170;
Matches 707; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy      79  GAAGGCTTTCTCTCGAGCGCGCGCTTTCGGCTTGGGGGGGGGTACAGCCCA 138
Db      19  GACGCGCTTCTCTCTGAGCGCGCGCGCTGTGGGGCGCGGGGGCGAGCCG 78
Qy      139  TCCATGACCATGGGCGCAAGAGAGCCGACAGGCCAAAGACAAAGCAAGCAACCTGCC 198
Db      79  TCCATGACCATGGGCGCAAGAGAGCCGACAGGCCAAAGACAAAGCAAGCAACCTGCC 138
Qy      199  GCAGACGAAGGGTTTGGGATTTGAGCTCTGCACTTTCAGAAAACAGTGTGAGCCCTT 258
Db      139  GCAGACGAAGGGTTTGGGATTTGAGCTCTGCACTTTCAGAAAACAGCGCCGAGCCCTT 198
Qy      259  AAATGCGAGCATCTCGATGTGAGAAAGGCACTCCACACAGAAAACCTCGATCAATCT 318
Db      199  AAATGCGAGCATCTCGATGTGCGAAAGGCACTCCACACAGAAAACCTCGCATCAATCT 258
Qy      319  CAGCTGTGGCACAACAAGTGGCACAACAGTATGCGACCCCAACCAACCCCTTAAAGAG 378
Db      259  CAGCTGTGGCACAACAGAGTGGCACAAGTATGCGCACTCCACCTTCCCTTAAAGAG 318
Qy      379  AAGAAGGAGAAAGTTGAAAAGCAGGACAAGAGAGAAACCTGAGAAAGCAAGAAATTAGT 438
Db      319  AAGAAGGAGAAAGTTCGAAAGCCCTGACAAGAAAAGCCAGAGAAAAGCAAGACATTAGC 378
Qy      439  CCTAGTGTACCAAGAAAATACCAACAGAAAACCAACCAAGATCTGACATTTCTGAAA 498
Db      379  CCCAGTGTCAACAAAGAAAACCAACCAAGAAAACCAAAAGTCTGTATTTCTGAAA 438
Qy      499  GATCTCTCTAGTGAAGCAACACAGCATACAGTCTGCAATGCTACAAACAGACACAGGAA 558
Db      439  GATCTCTCTAGTGAAGCTTACAGCATACAGTCTGCTTAACGCTACACAAAGACACAGGAA 498
Qy      559  ACAAAATCACACCTCAAGGCCCGGCTGAAAACCTGACAGGAGCATGTGCAAGAGTTG 618
Db      499  ACAAAACACACCTCAAGGCCCGGCTGAAGAAATGTGGACAGGACACCGCACAGCAGTTG 558
Qy      619  GCAGTAACTGTGGCAACGTCACCGTCACTTATTCAGACATTTTAAGGAAAGACTCGCTCC 678
Db      559  GCAGTAACTGTGGCAACGTCACCGTCACTTATTCAGACATTTTAAGGAAAGACTCGCTCC 618
Qy      679  TCATCGACATCTCTCATCCACAGTGCACCTCCAGTGCAGGGTCAGAACAGCAACAGAGC 738
Db      619  TCCTCCACATCTCTTCCACAGTGCACCTCCAGTGCAGGGTCAGAACAGCAACAGAGC 678
Qy      739  AGCTCGGGGTGAGAGACACAGAAGGGCTCTCCCGTTCTCCAGCCCAAGAGGGCGAC 798
Db      679  AGCTCGGGGTGAGAGACACAGAAGAGGGCTCTCTCCCGCTCTCTCCAGCCCAAGAGGGCGAC 738
Qy      799  ATGTGACAGTCAATGATGATCTTTGTGAATTTGCACATGGAATTTGTGAAA 850
Db      739  ATGTGACAGTGAATGATGATCTTTCTGAGATTTGCACATGGAATTTGTGACA 790
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RESULT 10
BG827273
LOCUS       BG827273               870 bp      mRNA      linear      EST 22-MAY-2001
DEFINITION  602749436P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4902201 5',
            mRNA sequence.
ACCESSION   BG827273
VERSION     BG827273.1   GI:14174860
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 870)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1CM1798 row: h column: 10
            High quality sequence stop: 774.
            Location/Qualifiers
              1..870
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4902201"
                /tissue_type="thadomyosarcoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 17"
                /note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
                Site 2: XhoI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 58.3%; Score 659.2; DB 4; Length 870;
Best Local Similarity 96.5%; Pred. No. 3.8e-168;
Matches 748; Conservative 0; Mismatches 19; Indels 8; Gaps 7;

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QY       75  CCACGAGGCGTTTCCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 134
DB        |||
QY       135  CCATCCATGACCATGGCGGCAAGAAGACCGCGACCA-GGCCAAAAAGACAAGCGAAAC 193
DB        |||
QY       147  CCATCCATGACCATGGCGGCAAGAAGACCGCGACCATGGCCAAAAAGACAAGCGAAAC 206
QY       194  CTGCCGCGACGACGAGGGTTTTGGATTGTAGCGTCTGCACCTTCGAAAAACAGTGTGGAAG 253
DB        |||
QY       207  CTGCCGCGACGACGAGGGTTTTGGATTGTAGCGTCTGCACCTTCGAAAAACAGTGTGGAAG 266
QY       254  CTTTAAATGCAGCATCTCGATGTGAGGAAGGACCTCCACCGAAAAACCTCGGATCA 313
DB        |||
QY       267  CTTTAAATGCAGCATCTCGATGTGAGGAAGGACCTCCACCGAAAAACCTCGGATCA 326
QY       314  ATTCTCAGCTGGTGGCACAACAGTGGCACAACAGTATGCCCCACCCACCCCTTAAAA 373
DB        |||
QY       327  ATTCTCAGCTGGTGGCACAACAGTGGCACAACAGTATGCCCCACCCACCCCTTAAAA 386
QY       374  AGGAGAAGAGGAGAAGTTGAAAGCAGGACCAAGAGAAACCTGTGAAAGACAAGGAAA 433
DB        |||
QY       387  AGGAGAAGAGGAGAAGTTGAAAGCAGGACCAAGAGAAACCTGTGAAAGACAAGGAAA 446
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434  TTAGTCTCTAGTGTTCACCAAGAAAAAATACCAACAAGAAAAACCAAAAGTCTGACATTC 493
447  TTAGTCTCTAGTGTTCACCAAGAAAAAATACCAACAAGAAAAACCAAAAGTCTGACATTC 506
494  TGAAGATCTCTCTAGTGTGAGCAACCAAGCAATACAGTCTGCAAAATGCTTACAACA-AGACC 552
507  TGAAGATCTCTCTAGTGTGAGCAACCAAGCAATACAGTCTGCAAAATGCTTACAACAAGACC 566
553  AGCAAAACAAATCACACCTCAAGGCCCGGCTGAAAAACGTTGGAGCAGGACATGCAACAG 612
567  AGCAAAACAAATCACACCTCAAGGCCCGGCTGAAAAACGTTGGAGCAGGACATGCAACAG 626
613  CAGTTGGCAGTAATCTGTGGGCAACGTCACCTCA-TTATCACAGACTTTAAGGA-AGA 670
627  CAGTTGGCAGTAATCTGTGGGCAACGTCACCTCA-TTATCACAGACTTTAAGGA-AGA 686
671  CTCGCTCC-TCATCGACATCTCTATCCACAGTACCTCCAGTGCAGGGTTCAGAACAGCAG 729
687  CTCGCTCC-TCATCGACATCTCTATCCACAGTACCTCCAGTGCAGGGTTCAGAACAGCAG 746
730  AACCAGA--GCAGCTCGGGGTTCAGAGACACA-GACAAGGGCTCTCCCGTTCTCCACG 786
747  AACCAGAAGCAGCATCGGGGTTCAGAGACACA-GACAAGGGCTCTCTCAGTTACTCCAG 806
787  CCAAAGGCGCAGATGTCTCAGCAGTCAATGATCAATCTTTGTGAAATTCACATGGA 841
807  GCAAAGGCGCAGATGTCTCAGCAGTCAATGATCAATCTTTCTGAAATTCACCATGGA 861
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RESULT 11
CK777039/c
LOCUS CK777039 726 bp mRNA linear EST 20-FEB-2004
DEFINITION 964031 MARC 2BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CK777039
VERSION CK777039.1 GI:42729352
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 726)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Cassas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A.,
Chitko-McKown,C.G., Perteau,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
JOURNAL 21180013
MEDLINE 11282978
PUBMED
COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smithemail.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: 120 row: A column: 12
 Seq primer: GTAATACGACTCACTATAGG.
 Location/Qualifiers
 1..726
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 2BOV"
 /note="Vector: pCMV SPOR76; Site_1: NotI; Site_2: SalI;


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QY 775 CGTTCCTCAGCCCAAGGGGACATGTGACAGTCAATGATGATCTTTGTGA 828
Db |||||||
601 CGTTCCTCAGCCCAAGGGGACATGTGACAGTCAATGATGATCTTTGTGA 654

RESULT 13
BQ015219/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ015219 662 bp mRNA linear EST 26-MAR-2002
UI-H-ED1-axw-f-13-0-UI.s1 NCI_CGAP_Ed1 Homo sapiens cDNA clone
IMAGE:5834508 3', mRNA sequence.
BQ015219
BQ015219.1 GI:19740120
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 662)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 1-23, >AT-rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1. 662
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5834508"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ed1"
/note="Organ: Left Pubic Bone, Vector: p77T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP Ed1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C85. The library was constructed according to
Bonald, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into p77T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dfr)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_TISSUE=chondrosarcoma
TAG_LiB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"

ORIGIN
Query Match 57.0%; Score 645.2; DB 5; Length 662;
Best Local Similarity 99.4%; Pred. No. 2.3e-164;
Matches 647; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 453 GAAATATACCAACAGAAACCAAAAGTCTGACATCTTGAAGATCTCTTAGTGA 512
Db |||||||
662 GAAATATACCAACAGAAACCAAAAGTCTGACATCTTGAAGATCTCTTAGTGA 603
QY 513 AGCAACAGCATACATCTGCAATGCTACACAAAGACCGGAAACAAATCACACCTC 572
```

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Db |||||||
602 AGCAACAGCATACATCTGCAATGCTACACAAAGACCGGAAACAAATCACACCTC 543
QY |||||||
573 AAGSCCCCGGCTGAAAACAGTGGACAGGACACTGCACAGCAGTTGGCAGTAACTGTGGG 632
Db |||||||
542 AAGSCCCCGGCTGAAAACAGTGGACAGGACACTGCACAGCAGTTGGCAGTAACTGTGGG 483
QY |||||||
633 CAACGTCACCGTCATTATTCACAGACTTTTAAGGAAAAGACTCGCTCCTCATCGACATCCTC 692
Db |||||||
482 CAACGTCACCGTCATTATTCACAGACTTTTAAGGAAAAGACTCGCTCCTCATCGACATCCTC 423
QY |||||||
693 ATCCACAGTGAACCTCCAGTGCAGGCTCAGAACACAGACAGACCTCGGGGTGAGA 752
Db |||||||
422 ATCCACAGTGAACCTCCAGTGCAGGCTCAGAACACAGACAGACCTCGGGGTGAGA 363
QY |||||||
753 GAGCACAGACAAAGGGCTCCTCCGCTTCTCCACGCCAAAGGGCGACATGTTCAGCAGTCAA 812
Db |||||||
362 GAGCACAGACAAAGGGCTCCTCCGCTTCTCCACGCCAAAGGGCGACATGTTCAGCAGTCAA 303
QY |||||||
813 TGATGAATCTTTGTGAAATTGACATGGAATTGTGAAAACCTATGAATCAGGGTATGAAAT 872
Db |||||||
302 TGATGAATCTTTGTGAAATTGACATGGAATTGTGAAAACCTATGAATCAGGGTATGAAAT 243
QY |||||||
873 TCAAAAACCTCACCTGCCCATGCTGCTTGCATCCTCGAGAAATCTTCTGTGGACATCGAC 932
Db |||||||
242 TCAAAAACCTCACCTGCCCATGCTGCTTGCATCCTCGAGAAATCTTCTGTGGACATCGAC 183
QY |||||||
933 CTCTTAGTGAGTGCAGGAGTAATTTCTGCTGCATGGGCATCTGCCCAACCAAGGAAT 992
Db |||||||
182 CTCTTAGTGAGTGCAGGAGTAATTTCTGCTGCATGGGCATCTGCCCAACCAAGGAAT 123
QY |||||||
993 TTGCGACCTCAGCAGTACTCTTGCACATTTTATGTATTCATTTATATGATTTTC 1052
Db |||||||
122 TTGCGACCTCAGCAGTACTCTTGCACATTTTATGTATTCATTTATATGATTTTC 63
QY |||||||
1053 CTACAATCATTTATATTTGATGATGCTCCTCGAATCTCTTTTATATATAAAA 1103
Db |||||||
62 CTACAATCATTTATATTTGATGATGCTCCTCGAATCTCTTTTATATATAAAA 12

RESULT 14
CK299391 664 bp mRNA linear EST 15-DEC-2003
UI-E-EJ1-ajv-e-08-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
DEFINITION
UI-E-EJ1-ajv-e-08-0-UI 3', mRNA sequence.
ACCESSION
CK299391
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 664)
Bonald, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Greg Hageman
cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/eye.html
The following repetitive elements were found in this cDNA
```


AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GPC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match	55.5%;	Score 628;	DB 5;	Length 650;
Best Local Similarity	99.1%;	Pred. No. 1.1e-159;		
Matches 631;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	467	AGAAACCAAACTGAGTCTGAAAGATCTCTCTAGTGAAGCAACACGATAC	526
Db	1	AGAAACCAAACTGAGTCTGAAAGATCTCTCTAGTGAAGCAACACGATAC	60
QY	527	AGTCTGCAATGCTACAAAGAGACGAGCAACAAATCACACCTCAAGGCCCGGCTGA	586
Db	61	AGTCTGCAATGCTACAAAGAGACGAGCAACAAATCACACCTCAAGGCCCGGCTGA	120
QY	587	AAAACTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACTGTGGGCAACGTCAACGTC	646
Db	121	AAAACTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACTGTGGGCAACGTCAACGTC	180
QY	647	TTATCACAGCTTTAAGGAAAAGACTCGCTCTCTATCGACATCTCCATCCACAGTGACCT	706
Db	181	TTATCACAGCTTTAAGGAAAAGACTCGCTCTCTATCGACATCTCCATCCACAGTGACCT	240
QY	707	CCAGTGCAGGGTCAGAACAGCAGACAGCAGAGCTCGGGGTCAGAGAGCAGACAAAG	766
Db	241	CCAGTGCAGGGTCAGAACAGCAGACAGCAGAGCTCGGGGTCAGAGAGCAGACAAAG	300
QY	767	GCTCTCTCCGTTCTCCAGCCAAAGGGCGACATGTGACAGTCAATGATGAATCTTTGT	826
Db	301	GCTCTCTCCGTTCTCCAGCCAAAGGGCGACATGTGACAGTCAATGATGAATCTTTGT	360
QY	827	GAAATGCAATGGAATGTGAAAATATGAAATCAGGGTATGAAATTCAAAACCTCCACC	886
Db	361	GAAATGCAATGGAATGTGAAAATATGAAATCAGGGTATGAAATTCAAAACCTCCACC	420
QY	887	TGCCCATGCTGTGATCCCTGGAGATCTTCTGTGGACATCGACCTCTTAGTGATGCT	946
Db	421	TGCCCATGCTGTGATCCCTGGAGATCTTCTGTGGACATCGACCTCTTAGTGATGCT	480
QY	947	GCCAGGATAATTTCTGCTTGGCATGGGATCTGGCCCAAGGAATTCGCACCCCTGACG	1006
Db	481	GCCAGGATAATTTCTGCTTGGCATGGGATCTGGCCCAAGGAATTCGCACCCCTGACG	540
QY	1007	ATTACTCTTGACACTTTTATGATTCATTTGTTTATGATTTTCTTAACAATCATTTA	1066
Db	541	ATTACTCTTGACACTTTTATGATTCATTTGTTTATGATTTTCTTAACAATCATTTA	600
QY	1067	TAATTGGATGCTCTCTGATCTACTTTTATATAAA	1103
Db	601	TAATTGGATGCTCTCTGATCTACTTTTATATAAA	637

Search completed: September 11, 2005, 15:26:48
Job time : 4314.65 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 09:29:36 ; Search time 218.254 Seconds
(without alignments)
8479.259 Million cell updates/sec

Title: US-09-655-109A-5

Perfect score: 11

Sequence: 1 tataactatctattcgatga.....tggcctcgagagatctatga 1131

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: .1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *

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1: /cqn2 6/ptodata/1/ina/5A COMB.seq:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.se

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
c	1	152.6	13.5	376	4	US-09-513-999C-3095	Sequence 3095, Appl
	2	106.6	9.4	466	4	US-09-621-976-2061	Sequence 2061, Appl
	3	74	6.5	1039	3	US-09-269-617-11	Sequence 11, Appl
	4	73	6.5	231	3	US-09-012-515A-20	Sequence 20, Appl
	5	73	6.5	231	3	US-08-360-144A-20	Sequence 20, Appl
	6	73	6.5	231	3	US-09-012-504A-20	Sequence 20, Appl
	7	73	6.5	231	3	US-09-012-399A-20	Sequence 20, Appl
	8	73	6.5	231	5	PCT-US95-06722-20	Sequence 20, Appl
	9	71	6.3	1025	3	US-09-269-617-13	Sequence 13, Appl
	10	59.2	5.2	7218	1	US-08-232-463-14	Sequence 14, Appl
c	11	56.8	5.0	288	3	US-09-025-151-29	Sequence 29, Appl
	12	56.8	5.0	288	4	US-09-637-240-29	Sequence 29, Appl
	13	55.8	4.9	1206	1	US-08-318-947A-1	Sequence 1, Appl
	14	55.8	4.9	1206	2	US-08-795-303-1	Sequence 1, Appl
	15	55	4.9	612	4	US-09-620-312D-529	Sequence 529, Appl
	16	55	4.9	659	4	US-09-620-312D-634	Sequence 634, Appl
	17	55	4.9	668	4	US-09-620-312D-198	Sequence 198, Appl
	18	55	4.9	771	4	US-09-620-312D-1043	Sequence 1043, Appl
	19	55	4.9	771	4	US-09-620-312D-1043	Sequence 1043, Appl
	20	55	4.9	783	4	US-09-620-312D-701	Sequence 701, Appl
c	21	55	4.9	827	4	US-09-620-312D-522	Sequence 522, Appl
	22	55	4.9	1163	4	US-09-620-312D-250	Sequence 250, Appl
	23	55	4.9	1196	4	US-09-620-312D-906	Sequence 906, Appl
	24	55	4.9	1239	4	US-09-620-312D-663	Sequence 663, Appl
	25	55	4.9	1239	4	US-09-620-312D-663	Sequence 663, Appl
	26	55	4.9	1477	4	US-09-620-312D-627	Sequence 627, Appl
	27	55	4.9	1572	4	US-09-620-312D-886	Sequence 886, Appl

RESULT 1

```

US-09-513-999C-3095
; Sequence 3095, Application US/095139995C
;
; Patent No. 6783361
;
; GENERAL INFORMATION:
;
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
;
; TITLE OF INVENTION: Expressed Sequence
;
; Patent No. 6783361
;
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,
; CURRENT FILING DATE: 2000-02-24
;
; PRIOR APPLICATION NUMBER: US 60/122,48
; PRIOR FILING DATE: 1999-02-26
;
; NUMBER OF SEQ ID NOS: 36681
;
; SOFTWARE: Patent.pm
;
; SEQ ID NO 395
;
; LENGTH: 376

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ALIGNMENTS

	28	55	4.9	1670	4	US-09-620-312D-177	Sequence 177, App
	29	55	4.9	1674	4	US-09-620-312D-593	Sequence 593, App
	30	55	4.9	1748	4	US-09-620-312D-60	Sequence 60, Appl
	31	55	4.9	1882	4	US-09-620-312D-172	Sequence 172, App
C	32	55	4.9	1956	4	US-09-620-312D-68	Sequence 68, Appl
	33	55	4.9	2064	4	US-09-620-312D-800	Sequence 800, App
	34	55	4.9	2123	4	US-09-620-312D-799	Sequence 799, App
	35	55	4.9	2295	4	US-09-620-312D-143	Sequence 143, App
	36	55	4.9	3289	4	US-09-620-312D-436	Sequence 436, App
C	37	55	4.9	3454	4	US-09-620-312D-167	Sequence 167, App
	38	55	4.9	3650	4	US-09-620-312D-30	Sequence 30, Appl
	39	55	4.9	3937	4	US-09-620-312D-280	Sequence 280, App
	40	55	4.9	4351	4	US-09-620-312D-347	Sequence 347, App
	41	55	4.9	4499	4	US-09-620-312D-678	Sequence 678, App
	42	55	4.9	4499	4	US-09-620-312D-679	Sequence 679, App
	43	55	4.9	4724	4	US-09-620-312D-677	Sequence 677, App
	44	55	4.9	4798	4	US-09-620-312D-298	Sequence 298, App
C	45	55	4.9	6378	4	US-09-620-312D-332	Sequence 332, App

ALIGNMENTS

RESULT 1

US-09-513-999C-3095

; Sequence 3095, Application US/09513999C

; Patent No. 6783961

GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 3095

; LENGTH: 376

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 69..374

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 367

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 100

; OTHER INFORMATION: Xaa=Lys or Thr

US-09-513-999C-3095

Query Match 13.5%; Score 152.6; DB 4; Length 376;

Best Local Similarity 66.7%; Pred. No. 7.3e-37;

Matches 218; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 125 CGGGGTACGCCCATCCATGACCATTGGCGGCAGACAGAGCCCCAGCCAGGCCCAAAAGAC 184

Dd 46 CGCGCTGCGGTGAATAGCCAAGCCATGGGAGACAAGAAGAGCCCCACAGGCCGGAAGCGGC 105

Qy 185 AAGCGAAACCTGCCGCAGACGAAGGTTTTTGGGATTGTAGCGTCTTGCACTTCAGAAACA 244

Dd 106 AGCCGAAGCGTCTCTCGATGAGGGTTACTGGGACTGTAGCGTCTGCACCTTCGGAACA 165

Qy 245 GTGCTGAAGCCTTTTAATGACGACATCTCGATGTGAGAAAGGACCTTCCACCGAAMAC 304

Dd 166 GCSCCGAGGCTTTCAGATGTGATGTCGATGTGCGAAGGGCACCTTCCACCGGGAAC 225


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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 128
; OTHER INFORMATION: /label= XhoI
US-09-012-515A-20

Query Match 6.5%; Score 73; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 60
DB 61 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 120

QY 61 TCGGATCCTCGAG 73
DB 121 TCGGATCCTCGAG 133

RESULT 6
US-09-012-504A-20
; Sequence 20, Application US/09012504A
; Patent No. 6464974
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, I.
; APPLICANT: Cottarel, G.
; APPLICANT: Damagnez, V.
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; FILE REFERENCE: APBI-P05-036
; CURRENT APPLICATION NUMBER: US/09/012,504A
; CURRENT FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 08/360,144
; PRIOR FILING DATE: 1994-12-20
; PRIOR APPLICATION NUMBER: 08/250,795
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Mammalian
US-09-012-504A-20

Query Match 6.5%; Score 73; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 60
DB 61 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 120

QY 61 TCGGATCCTCGAG 73
DB 121 TCGGATCCTCGAG 133

RESULT 7
US-09-012-399A-20
; Sequence 20, Application US/09012399A
; Patent No. 6509152
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, Maria Isabel
; APPLICANT: Chiu, Guillaume
; APPLICANT: Cottarel, Veronique
; APPLICANT: Damagnez, Veronique
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,399A

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Query Match          6.5%; Score 73; DB 5; Length 231;
Best Local Similarity 100.0%; Fred.No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCAACCCAAAAAAGAGATCTCGAAT 60
        |||||
Db       61 TATAACTATCTATTTCGATGATGAAGATACCCCAACCAACCCAAAAAAGAGATCTCGAAT 120

QY      61 TCGGATCCTCGAG 73
        |||||
Db       121 TCGGATCCTCGAG 133

RESULT 9
US-09-269-617-13
; Sequence 13, Application US/09269617
; Patent No. 6204253
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FACTORS THAT INTERACT WITH ONCOPROTEINS
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/269,617
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1025 base pairs

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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: B-lymphocyte
; IMMEDIATE SOURCE:
; LIBRARY: Human cdna library
; CLONE: SZ33
; US-09-269-617-13

Query Match          6.3%; Score 71; DB 3; Length 1025;
Best Local Similarity 92.4%; Pred.No. 2.9e-11;
Matches 85; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 TATAACTATCTATTTCGATGATGAAGATACCCACCAACCCCAAAAAAGAGATCTCGAAT 60
DB 35 TATAACTACCTATTTCGATGATGAAGATA-CCCAACCAACCCCAAAAAAGAGATCTCGAAT 93
QY 61 TCGGATCCTCGAGGCCACGAAGCCTTTCTCC 92
DB 94 TCGGATCCTCGAGGCCACGAANGCCGGCCTTC 125

RESULT 10
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500

```


GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,947A
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,530
; FILING DATE: 07-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A6462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-2920
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 172..648
; US-08-318-947A-1

Query Match 4.9%; Score 55.8; DB 1; Length 1206;
Best Local Similarity 84.0%; Pred. No. 1.7e-06;
Matches 63; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 31 CCACCAACCCAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCCTTCT 90
Db 1 CCACCAACCCAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCCTTCT 90

Qy 91 CTCCTCCGAGCGGCC 105
Db 61 CTCCTCCGAGCGGCC 75

RESULT 14
US-08-795-303-1
; Sequence 1, Application US/08795303
; Patent No. 5948656
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC

COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,303
FILING DATE: 04-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/318,947
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REFERENCE/DOCKET NUMBER: A6462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-2920
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1206 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 172..648
US-08-795-303-1

Query Match 4.9%; Score 55.8; DB 2; Length 1206;
Best Local Similarity 84.0%; Pred. No. 1.7e-06;
Matches 63; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 31 CCACCAACCCAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCCTTCT 90
Db 1 CCACCAACCCAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCCTTCT 90

Qy 91 CTCCTCCGAGCGGCC 105
Db 61 CTCCTCCGAGCGGCC 75

RESULT 15
US-09-620-312D-529
; Sequence 529, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides

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; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620.312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 529
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (118)..(486)
US-09-620-312D-529

Query Match      4.9%; Score 55; DB 4; Length 612;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAAAGAGATCT 55
        |||||||||||||||||||||||||||||||||||||||||||||||
Db      20 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAAAGAGATCT 74

Search completed: September 11, 2005, 15:33:26
Job time : 220.254 secs
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